GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 11, 2005, 18:24:45 ; Search time 41 Seconds
(without alignments)
1067.771 Million cell updates/sec

Title: US-09-943-664-50
Perfect score: 2529
Sequence: 1 MLHPETSPGRGHLLAVLLAL.....RNRYICQFAQEHISRWGPGS 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	250	9.9	245	2	S68691	neutrophil granule
2	236	9.3	1268	2	S52781	neurocan - mouse
3	232	9.2	219	2	JC4131	glioma pathogenesi
4	231	9.1	266	2	JC5308	testis-specific, v
5	224	8.9	312	2	T16415	hypothetical prote
6	221	8.7	243	2	B33329	cysteine-rich secr
7	213.5	8.4	249	2	S68684	cysteine-rich secr
8	212	8.4	1257	2	S28764	neurocan precursor
9	209	8.3	244	2	A49202	cysteine-rich secr
10	208	8.2	243	2	JE0204	testicular protein
11	200	7.9	2397	1	A55535	versican precursor
12	196	7.8	2409	1	A60979	versican precursor
13	193.5	7.7	243	2	A33329	testis-specific pr
14	191	7.6	3562	2	A47171	chondroitin sulfat
15	190	7.5	1643	2	T14274	versican precursor
16	190	7.5	3381	2	T42389	versican precursor
17	189.5	7.5	1455	1	A48925	mannose receptor p
18	189	7.5	207	2	T22436	hypothetical prote
19	188.5	7.5	246	2	A24609	acidic epididymal
20	187.5	7.4	205	2	F44583	venom allergen ant
21	185.5	7.3	161	2	JQ1693	pathogenesis-relat
22	185.5	7.3	212	2	T22437	hypothetical prote
23	184	7.3	162	2	T08154	pathogenesis-relat
24	184	7.3	202	2	H44583	venom allergen ant
25	182.5	7.2	159	1	VCTO14	pathogenesis-relat
26	181.5	7.2	177	2	T08126	pathogenesis-relat
27	180.5	7.1	159	2	S26238	pathogenesis-relat
28	180.5	7.1	163	2	T04989	pathogenesis-relat
29	180.5	7.1	205	2	A37329	antigen 5 - paper
30	179	7.1	184	2	S10205	pathogenesis-relat
31	178.5	7.1	1456	1	A36563	mannose receptor p
32	178	7.0	202	2	G44583	venom allergen ant
33	177.5	7.0	2825	2	T14271	Doc4 protein, stre
34	177	7.0	178	2	S68681	cysteine-rich secr
35	176.5	7.0	161	2	S65777	pathogenesis-relat
36	176	7.0	185	2	T10677	pathogenesis-relat
37	175	6.9	168	2	T07146	pathogenesis-relat
38	175	6.9	205	2	T48294	pathogenesis relat
39	175	6.9	208	2	T19852	hypothetical prote
40	174	6.9	168	2	C24620	pathogenesis-relat
41	174	6.9	204	2	A44583	venom allergen ant
42	173.5	6.9	212	2	T27834	hypothetical prote
43	173.5	6.9	213	2	T22439	hypothetical prote
44	173	6.8	209	2	T19848	hypothetical prote
45	173	6.8	883	2	S49126	brevican precursor
46	172	6.8	163	2	T02054	pathogenesis relat
47	172	6.8	164	2	T04299	pathogenesis-relat
48	171	6.8	140	2	A33155	pathogenesis-relat
49	171	6.8	168	2	A24620	pathogenesis-relat
50	170	6.7	175	2	S43894	pathogenesis-relat
51	170	6.7	2415	1	A39086	aggrecan precursor
52	169	6.7	204	2	B37329	antigen 5 - easter
53	169	6.7	2352	2	T30201	Notch homolog prot
54	168.5	6.7	912	2	A54423	brevican precursor
55	168.5	6.7	2321	2	S78549	notch3 protein - h
56	168	6.6	204	2	B44583	venom allergen ant
57	167	6.6	167	2	S14969	pathogenesis-relat
58	165	6.5	168	2	B24620	pathogenesis-relat
59	164.5	6.5	167	2	S51679	pathogenesis-relat
60	163	6.4	164	2	S37166	pathogenesis-relat
61	163	6.4	173	2	S47171	gene PR-1 protein
62	163	6.4	208	2	T20661	hypothetical prote
63	163	6.4	883	2	S57653	brevican precursor
64	163	6.4	2531	2	S18188	notch protein homo
65	162.5	6.4	2531	2	T31070	notch homolog - se
66	162	6.4	168	2	JC7330	acidic pathogenesi
67	162	6.4	241	2	B49202	cysteine-rich secr
68	161.5	6.4	207	2	T31959	hypothetical prote
69	161.5	6.4	213	2	B31085	antigen 5-3 precur
70	161.5	6.4	2524	2	A35844	Xotch protein - Af
71	161	6.4	330	2	T46256	brevican - human (
72	160.5	6.3	179	2	S22531	pathogenesis-relat
73	160	6.3	164	2	S39474	pathogenesis-relat
74	160	6.3	206	2	E44583	venom allergen ant
75	160	6.3	4006	2	T09070	probable tenascin
76	159.5	6.3	162	2	A96537	hypothetical prote
77	159.5	6.3	176	2	F84583	pathogenesis-relat
78	159	6.3	209	2	T19847	hypothetical prote
79	158.5	6.3	161	2	H84518	pathogenesis-relat
80	158.5	6.3	728	2	I50719	C-Delta-1 - chicke
81	158	6.2	164	2	S52627	pathogenesis-relat
82	158	6.2	722	2	I48324	DELTA-like 1 - mou
83	157	6.2	204	2	C44583	venom allergen ant
84	157	6.2	207	2	T22438	hypothetical prote
85	157	6.2	211	2	B58853	venom allergen Sol
86	157	6.2	227	2	A31085	antigen 5-2 precur
87	157	6.2	2531	2	A46019	notch-1 protein -
88	156.5	6.2	1574	2	T13954	MEGF6 protein - ra
89	156	6.2	2703	1	A24420	notch protein - fr
90	155.5	6.1	301	2	S13165	asialoglycoprotein
91	154.5	6.1	161	2	T52399	pathogenesis-relat
92	154.5	6.1	172	2	T04990	pathogenesis-relat
93	153.5	6.1	2318	2	S45306	notch 3 protein -
94	153	6.0	164	2	S52626	pathogenesis-relat
95	152	6.0	211	2	T19859	hypothetical prote
96	152	6.0	2109	1	I50421	aggrecan precursor
97	151	6.0	1064	2	A40136	fibropellin Ia - s
98	151	6.0	1429	2	S06434	homeotic protein l
99	150.5	6.0	174	2	S71554	pathogenesis-relat
100	150.5	6.0	280	2	T29200	hypothetical prote
101	150.5	6.0	301	1	LNRT2	hepatic lectin 2 -
102	150.5	6.0	3566	1	A40701	tenascin-X precurs

103	149	5.9	253	2	E89130
104	149	5.9	2437	2	S42612
105	148.5	5.9	166	2	S71270
106	148.5	5.9	1620	2	T27283
107	148	5.9	161	2	B96537
108	148	5.9	177	2	D84583
109	147.5	5.8	2139	2	A35672
110	147	5.8	1203	2	A49175
111	146	5.8	2555	2	A40043
112	145.5	5.8	205	2	D44583
113	145.5	5.8	210	2	T19849
114	145.5	5.8	283	2	D86143
115	145.5	5.8	1479	2	T42710
116	145	5.7	190	2	T04232
117	144.5	5.7	686	2	JC7569
118	144.5	5.7	782	2	A61625
119	144.5	5.7	1687	2	T30176
120	144.5	5.7	1964	2	T09059
121	143.5	5.7	212	2	B37330
122	143	5.7	881	2	S56032
123	143	5.7	2471	2	A49128
124	143	5.7	4135	2	T42629
125	142.5	5.6	306	2	A42230
126	142	5.6	207	2	T22432
127	142	5.6	210	2	T04233
128	141.5	5.6	214	2	S65052
129	141.5	5.6	1295	2	A32901
130	141	5.6	196	2	T27833
131	141	5.6	202	1	TTHUN
132	141	5.6	685	2	JC7570
133	141	5.6	1220	2	A56136
134	140.5	5.6	241	2	T33397
135	140	5.5	1746	1	S19694
136	139.5	5.5	284	2	S29855
137	138	5.5	550	2	A28166
138	138	5.5	1722	2	E89753
139	137.5	5.4	207	1	LNCHL
140	137.5	5.4	284	1	LNRTL
141	137.5	5.4	311	1	LNHU2A
142	137	5.4	299	2	S56031
143	136.5	5.4	570	2	A48836
144	136.5	5.4	1607	1	MMMSB2
145	136	5.4	147	2	A26697
146	136	5.4	3191	2	T22945
147	135.5	5.4	833	2	S19087
148	135.5	5.4	862	2	S43922
149	135.5	5.4	1458	1	A49707
150	135	5.3	173	2	S10548
151	135	5.3	198	2	T26861
152	134.5	5.3	742	2	JC7595
153	134.5	5.3	1124	1	I58388
154	134.5	5.3	1469	2	B36665
155	134.5	5.3	1480	2	A36665
156	134.5	5.3	3002	2	A47221
157	134	5.3	861	2	A48825
158	134	5.3	1523	2	T13953
159	133.5	5.3	832	2	A31246
160	133.5	5.3	880	2	S00670
161	133	5.3	1025	2	T42626
162	132	5.2	808	2	T23129
163	131.5	5.2	173	2	B47148
164	131.5	5.2	308	2	T29754
165	131.5	5.2	2019	1	JQ1322
166	131	5.2	383	2	S53716
167	131	5.2	798	2	A40526
168	130.5	5.2	155	2	S78774
169	130.5	5.2	1122	2	I54237
170	130.5	5.2	1123	1	JN0712
171	130.5	5.2	1125	1	JH0771
172	130.5	5.2	2201	2	A32160
173	130	5.1	223	2	B46467
174	130	5.1	1111	2	T26972
175	129.5	5.1	308	2	T29756

protein F52E1.2 [i
transmembrane prot
pathogenesis-relat
hypothetical prote
hypothetical prote
probable pathogene
crumbs protein - f
Motch B protein -
notch protein homo
venom allergen ant
hypothetical prote
hypothetical prote
mannose receptor,
pathogenesis-relat
Delta-4 protein -
tenascin-like prot
EGF repeat transme
notch4 - mouse
venom allergen III
probable membrane
cell-fate determin
tenascin-X - bovin
lectin M-ASGP-BP p
hypothetical prote
pathogenesis-relat
pistil-specific pr
glp1 protein precu
hypothetical prote
tetranectin precur
Delta-4 protein -
jagged protein pre
hypothetical prote
tenascin precursor
asialoglycoprotein
Kupffer cell recep
protein F11C7.4 [i
hepatic lectin - c
hepatic lectin - r
asialoglycoprotein
pathogenesis-relat
fibropellin C prec
laminin gamma-1 ch
echinoidin - sea u
hypothetical prote
gene Delta protein
versican - pig-tai
phospholipase A2 r
lectin - barnacle
hypothetical prote
scavenger receptor
protein-tyrosine k
slit protein 2 pre
slit protein 1 pre
fibrillin 1 precur
Notch homolog Motc
MEGF5 protein - ra
neurogenic protein
neurogenic repetit
secreted leucine-r
hypothetical prote
reg II, regenerati
hypothetical prote
tenascin precursor
delta-like homeoti
integrin beta-7 ch
perlucin - Halioti
protein-tyrosine k
protein-tyrosine k
protein-tyrosine k
tenascin-C - human
NKR-P1 protein hom
hypothetical prote
hypothetical prote

176	129.5	5.1	385	2	S53718
177	129.5	5.1	385	2	A54785
178	129.5	5.1	513	2	D88991
179	129.5	5.1	806	2	A46271
180	129.5	5.1	1810	1	A32230
181	129.5	5.1	2406	2	A54148
182	129.5	5.1	2515	2	S47008
183	129	5.1	1136	1	S57845
184	129	5.1	2824	2	T22759
185	128.5	5.1	1321	2	JE0352
186	128.5	5.1	1609	1	MMHUB2
187	128.5	5.1	3075	2	S14458
188	128	5.1	165	2	E84583
189	128	5.1	473	2	A56175
190	128	5.1	719	2	T00266
191	127.5	5.0	202	2	JC4031
192	127.5	5.0	379	2	A59180
193	126.5	5.0	161	2	E85354
194	126.5	5.0	331	1	LNMSER
195	126.5	5.0	385	2	T21763
196	126.5	5.0	1408	2	S16148
197	126.5	5.0	4391	2	A38096
198	126	5.0	1487	2	S48719
199	126	5.0	3623	2	T08618
200	125.5	5.0	463	2	T26655
201	125	4.9	135	2	A38609
202	125	4.9	1125	1	S57846
203	125	4.9	1463	2	A53210
204	124.5	4.9	309	1	S34198
205	124.5	4.9	374	1	A42046
206	124.5	4.9	384	2	T21929
207	124.5	4.9	1138	1	S24066
208	124.5	4.9	2918	2	A54105
209	124.5	4.9	4544	1	S02392
210	124	4.9	177	2	S04728
211	124	4.9	1353	1	JH0675
212	124	4.9	1372	2	T25933
213	123.5	4.9	1134	1	JN0711
214	123	4.9	166	1	RGHU1A
215	123	4.9	166	2	A45751
216	123	4.9	678	2	B48089
217	123	4.9	3084	1	MMMSA
218	122.5	4.8	166	1	A37289
219	122.5	4.8	304	2	JX0209
220	122	4.8	1723	2	S58880
221	122	4.8	2823	2	F87908
222	122	4.8	2823	2	T23064
223	122	4.8	2871	2	A55567
224	122	4.8	3102	2	T43291
225	121.5	4.8	308	2	JC7125
226	121.5	4.8	601	2	T22025
227	121.5	4.8	601	2	D89711
228	121.5	4.8	1356	2	A45445
229	121.5	4.8	1639	1	MMFFB2
230	121.5	4.8	2014	2	T21560
231	121.5	4.8	2871	2	A55624
232	121.5	4.8	3623	2	T09456
233	121	4.8	166	1	RGHU1B
234	121	4.8	220	2	C46467
235	121	4.8	237	2	JC5309
236	121	4.8	293	2	B26637
237	121	4.8	404	2	A46274
238	121	4.8	933	2	A31930
239	121	4.8	2531	2	T16743
240	120.5	4.8	1808	2	T15099
241	120.5	4.8	2180	2	T29764
242	120.5	4.8	2907	2	A57278
243	120	4.7	835	2	JP0076
244	120	4.7	1340	2	A39808
245	120	4.7	2124	2	A28452
246	120	4.7	2327	2	T42630
247	119.5	4.7	738	2	S40992
248	119.5	4.7	739	2	B88553

homeotic protein d
preadipocyte facto
protein apx-1 [imp
integrin beta-7 ch
tenascin precursor
odz protein - frui
tenascin-like prot
protein-tyrosine k
hypothetical prote
mucin MUC5B, trach
laminin gamma-1 ch
laminin alpha-1 ch
probable pathogene
adhesive plaque pr
hypothetical prote
tetranectin precur
Wnt inhibitory fac
PR-1-like protein
IgE Fc receptor, l
hypothetical prote
gene serrate prote
perlecan precursor
phospholipase-A(2)
intrinsic factor-B
hypothetical prote
lectin, galactose-
protein-tyrosine k
phospholipase A2 r
IgE Fc receptor II
surfactant protein
hypothetical prote
protein-tyrosine k
fibrillin-2 precur
alpha-2-macroglobu
pathogenesis-relat
restrictin precurs
hypothetical prote
protein-tyrosine k
regenerating islet
pancreatic stone p
growth arrest-spec
laminin alpha-1 ch
tetranectin homolo
lectin, galactose/
receptor DEC-205 -
protein T22A3.8 [i
hypothetical prote
fibrillin I - bovi
laminin alpha chai
epidermal growth f
hypothetical prote
protein F40E10.4 [
janusin precursor,
laminin gamma-1 ch
hypothetical prote
fibrillin-1 precur
intrinsic factor-B
regenerating islet
NKR-P1 protein hom
testis-specific, v
neurogenic repetit
HIV gp120-binding
cytotactin - chick
hypothetical prote
hypothetical prote
hypothetical prote
fibrillin-2 precur
nel protein - chic
proteoglycan core
proteoglycan core
aggrecan - bovine
hypothetical prote
protein K04H4.2b [

249	119.5	4.7	1584	2	T00026	brain-specific ang
250	119.5	4.7	4545	1	S25111	alpha-2-macroglobu
251	119	4.7	616	2	T29234	hypothetical prote
252	119	4.7	661	2	T42754	hypothetical prote
253	118.5	4.7	259	2	T21011	hypothetical prote
254	118.5	4.7	293	2	T09065	hypothetical prote
255	118.5	4.7	551	2	I46709	endothelial leukoc
256	118.5	4.7	555	2	T21028	hypothetical prote
257	118.5	4.7	1700	2	S08167	Balbiani ring 3 pr
258	118.5	4.7	3106	1	S53868	laminin alpha-2 ch
259	118	4.7	140	2	JC7786	lectin CEL-I, N-ac
260	118	4.7	180	2	JX0347	acrosomal major pr
261	118	4.7	781	2	S43534	integrin beta3 - c
262	118	4.7	2214	2	T16305	hypothetical prote
263	117.5	4.6	378	2	B59180	Wnt inhibitory fac
264	117.5	4.6	1299	2	T43251	furin (EC 3.4.21.7
265	117.5	4.6	1531	2	T42218	slit-1 protein hom
266	117.5	4.6	1801	1	MMRTS	laminin beta-2 cha
267	117	4.6	165	2	A47148	reg I, regeneratin
268	117	4.6	2132	1	A55182	aggrecan precursor
269	117	4.6	2229	2	T16199	hypothetical prote
270	116.5	4.6	162	1	LNRC1	lectin BRA3-1 prec
271	116.5	4.6	162	1	LNRC3	lectin BRA3-2 prec
272	116.5	4.6	647	2	A43902	tenascin - eastern
273	116.5	4.6	1798	2	S53869	laminin beta-2 cha
274	116	4.6	321	1	LNHUER	IgE Fc receptor II
275	116	4.6	535	2	T19706	hypothetical prote
276	115	4.5	252	2	T46247	hypothetical prote
277	115	4.5	545	2	T18714	hypothetical prote
278	115	4.5	723	2	PN0509	integrin beta-3 ch
279	114.5	4.5	400	2	T46383	hypothetical prote
280	114.5	4.5	788	2	I51530	integrin beta-3 su
281	114.5	4.5	1326	2	B56395	secretory phosphol
282	114.5	4.5	1465	2	A56395	secretory phosphol
283	114	4.5	155	2	T28945	hypothetical prote
284	114	4.5	289	2	T22834	hypothetical prote
285	114	4.5	593	1	GYHU	granulin precursor
286	114	4.5	799	2	A38308	integrin beta-5 ch
287	113.5	4.5	575	1	THHUB	thrombomodulin pre
288	113.5	4.5	1291	2	T21694	hypothetical prote
289	113	4.5	589	2	T43210	fibulin-1D precurs
290	113	4.5	680	2	PN0510	integrin beta-3 ch
291	113	4.5	689	2	T42760	fibulin, splice fo
292	113	4.5	712	2	T42990	fibulin 1, splice
293	112.5	4.4	907	2	T27317	hypothetical prote
294	112	4.4	165	2	A28351	pancreatic stone p
295	112	4.4	321	2	T26152	hypothetical prote
296	112	4.4	656	2	JC2005	integrin beta-5 ch
297	112	4.4	1557	2	T28811	hypothetical prote
298	112	4.4	1737	2	T00209	MEGF8 protein - hu
299	111	4.4	379	2	T16213	APX-1 protein homo
300	111	4.4	3034	2	T14119	seven-pass transme
301	110.5	4.4	180	2	JX0349	acrosomal major pr
302	110.5	4.4	502	2	T21935	hypothetical prote
303	110.5	4.4	640	2	T08179	LRG5 protein - Chl
304	110	4.3	264	2	T16271	hypothetical prote
305	110	4.3	329	2	S38082	pathogenesis-relat
306	110	4.3	375	1	A45225	pulmonary surfacta
307	110	4.3	379	2	T27350	hypothetical prote
308	110	4.3	387	2	B49175	Motch A protein -
309	110	4.3	1364	2	T00250	MEGF2 protein - hu
310	110	4.3	3871	2	T22812	hypothetical prote
311	110	4.3	4307	2	T20721	hypothetical prote
312	109.5	4.3	248	1	LNHUP1	pulmonary surfacta
313	109.5	4.3	248	1	LNHUPS	pulmonary surfacta
314	109.5	4.3	248	1	LNHUP6	pulmonary surfacta
315	109.5	4.3	644	1	A40212	uromodulin precurs
316	109.5	4.3	644	2	I84634	Tamm-Horsfall prot
317	109.5	4.3	803	1	IJCH3	integrin, band 3 p
318	109.5	4.3	1748	1	JN0786	integrin beta-4 ch
319	109.5	4.3	1895	2	T06609	disease resistance
320	109	4.3	753	2	B36268	platelet glycoprot
321	109	4.3	778	2	A60798	platelet glycoprot
322	109	4.3	788	2	I77349	platelet glycoprot
323	109	4.3	1895	2	T15881	hypothetical prote
324	109	4.3	3707	2	S18252	heparan sulfate pr
325	108.5	4.3	1101	2	T16840	hypothetical prote
326	108	4.3	293	2	T22919	hypothetical prote
327	108	4.3	603	2	S28941	coagulation factor
328	108	4.3	773	2	I46059	beta-1 integrin su
329	108	4.3	1450	2	T30273	hypothetical prote
330	107.5	4.3	166	2	T28809	hypothetical prote
331	107.5	4.3	248	2	I51921	pulmonary surfacta
332	107.5	4.3	308	2	B88392	protein R06B10.3 [
333	107.5	4.3	577	2	A60501	thrombomodulin pre
334	107.5	4.3	577	2	B37057	integrin beta-6 ch
335	107.5	4.3	769	1	IJHULM	leukocyte adhesion
336	107.5	4.3	2610	2	T20968	hypothetical prote
337	107.5	4.3	3712	2	S18253	laminin alpha-1 ch
338	107.5	4.3	4543	1	A53102	alpha-2-macroglobu
339	107	4.2	295	2	T28078	hypothetical prote
340	107	4.2	476	2	T32032	hypothetical prote
341	107	4.2	788	2	A26547	platelet glycoprot
342	106.5	4.2	142	2	S78596	ovocleidin - chick
343	106.5	4.2	163	1	A34313	antifreeze protein
344	106.5	4.2	174	2	I83377	regenerating prote
345	106.5	4.2	214	2	S27449	Scl4 protein - bra
346	106.5	4.2	256	2	JQ0708	lipopolysaccharide
347	106.5	4.2	375	2	T33797	hypothetical prote
348	106.5	4.2	655	1	A46688	hepatocyte growth
349	106.5	4.2	799	2	JC4126	integrin beta olig
350	106	4.2	227	2	A46467	natural killer cel
351	106	4.2	412	2	S72579	hypothetical prote
352	106	4.2	615	1	KFHU12	coagulation factor
353	106	4.2	1827	2	T34288	hypothetical prote
354	106	4.2	3672	2	T23433	hypothetical prote
355	106	4.2	3704	2	T37316	probable laminin a
356	105.5	4.2	160	2	T24764	hypothetical prote
357	105.5	4.2	283	1	LNFHLS	lectin precursor -
358	105.5	4.2	810	2	T10756	Nel-homolog protei
359	105.5	4.2	984	2	T00326	hypothetical prote
360	105.5	4.2	1522	2	T00028	brain-specific ang
361	105.5	4.2	3635	2	T10053	laminin alpha 5 ch
362	105	4.2	160	2	D85077	probable pathogene
363	105	4.2	961	1	TSHUP4	thrombospondin 4 p
364	105	4.2	1373	2	JE0095	gastric mucin MUC5
365	104.5	4.1	204	2	T32062	hypothetical prote
366	104.5	4.1	223	2	T21930	hypothetical prote
367	104.5	4.1	372	2	T29359	hypothetical prote
368	104.5	4.1	427	2	JC4915	ags protein precur
369	104.5	4.1	454	2	T26654	hypothetical prote
370	104.5	4.1	601	2	T34396	hypothetical prote
371	104.5	4.1	1221	2	A49457	fibulin-2 precurso
372	104.5	4.1	1820	2	A55494	latent transformin
373	104	4.1	211	2	T32590	hypothetical prote
374	104	4.1	380	2	T28081	hypothetical prote
375	104	4.1	809	2	A57283	integrin beta chai
376	104	4.1	1069	2	T42681	hypothetical prote
377	104	4.1	1914	2	T42635	tenascin Y precurs
378	104	4.1	5376	2	T42215	zonadhesin - mouse
379	103.5	4.1	251	2	A55035	cysteine-rich prot
380	103.5	4.1	369	2	S33603	surfactant protein
381	103.5	4.1	379	2	T22392	hypothetical prote
382	103.5	4.1	768	2	B41029	integrin beta-8 ch
383	103.5	4.1	799	1	IJMSFB	fibronectin recept
384	103.5	4.1	813	2	T21192	hypothetical prote
385	103.5	4.1	1193	2	A44018	laminin B2t chain
386	103.5	4.1	1790	1	MMFFB1	laminin beta-1 cha
387	103	4.1	612	2	B42755	E-selectin precurs
388	103	4.1	640	2	T19346	hypothetical prote
389	103	4.1	788	2	A37057	integrin beta-6 ch
390	103	4.1	1149	2	I38006	M130 antigen precu
391	103	4.1	1151	2	I38004	M130 antigen precu
392	103	4.1	1156	2	I38005	M130 antigen precu
393	102.5	4.1	102	2	B55885	chondroitin sulfat
394	102.5	4.1	461	1	KXHU	protein C (activat

395	102.5	4.1	570	2	T37314	probable kexin (EC
396	102.5	4.1	798	2	S01659	integrin beta-1 ch
397	102.5	4.1	798	2	B27079	fibronectin recept
398	102.5	4.1	915	2	T21773	hypothetical prote
399	102.5	4.1	927	2	T21772	hypothetical prote
400	102.5	4.1	1188	2	D86236	protein F14N23.5 [
401	102	4.0	964	2	JC5545	integrin beta-4 pr
402	102	4.0	1875	2	A36429	integrin beta-4 ch
403	101.5	4.0	301	2	A53570	collectin-43 - bov
404	101.5	4.0	628	2	T02602	vacuolar sorting r
405	101.5	4.0	642	1	S52111	uromodulin precurs
406	101.5	4.0	798	2	T22793	hypothetical prote
407	101	4.0	463	1	A36479	milk fat globule m
408	101	4.0	527	2	JE0373	low density lipopr
409	101	4.0	673	2	A48089	growth arrest-spec
410	101	4.0	770	2	S04847	leukocyte adhesion
411	101	4.0	771	2	A45839	leukocyte adhesion
412	101	4.0	792	2	F88656	protein F56D6.1 [i
413	101	4.0	1807	2	JC6319	integrin beta-4 ch
414	101	4.0	2704	2	S09118	G surface protein
415	101	4.0	4302	2	A38971	polycystic kidney
416	100.5	4.0	246	2	T24493	hypothetical prote
417	100.5	4.0	424	2	S11676	spore coat protein
418	100	4.0	148	2	JX0348	acrosomal major pr
419	100	4.0	425	2	C89753	protein F11C7.3 [i
420	100	4.0	483	2	T24856	hypothetical prote
421	100	4.0	2195	2	T34264	hypothetical prote
422	99.5	3.9	546	2	JC4798	seizure-related me
423	99.5	3.9	640	1	A30452	uromodulin precurs
424	99.5	3.9	1572	2	T00027	brain-specific ang
425	99.5	3.9	1751	1	MMHUMH	laminin alpha-2 ch
426	99.5	3.9	2476	2	T34022	zonadhesin - pig
427	99	3.9	177	2	A37408	betacellulin precu
428	99	3.9	322	2	T16633	hypothetical prote
429	99	3.9	409	2	T11743	pP47 protein - pig
430	99	3.9	475	1	EXCH	coagulation factor
431	99	3.9	520	2	G88846	protein T12A7.2 [i
432	99	3.9	610	2	A35046	E-selectin precurs
433	99	3.9	965	2	S62935	hypothetical prote
434	98.5	3.9	174	1	A48689	pancreatitis-assoc
435	98.5	3.9	234	1	S15102	eosinophil major b
436	98.5	3.9	387	2	I38449	extracellular prot
437	98.5	3.9	628	2	T02604	probable vacuolar
438	98.5	3.9	1797	2	A55677	laminin beta-2 cha
439	98	3.9	417	2	T20199	hypothetical prote
440	98	3.9	426	2	D88103	protein W10G11.6 [
441	98	3.9	461	1	JX0210	protein C (activat
442	98	3.9	887	2	T11566	envelope glycoprot
443	98	3.9	922	2	T37256	metalloproteinase
444	98	3.9	2910	2	T42214	otogelin - mouse
445	97.5	3.9	1106	2	T18739	hypothetical prote
446	97.5	3.9	2718	2	A23475	G surface protein
447	97	3.8	172	2	S32489	lectin - Iberian r
448	97	3.8	275	2	T21933	hypothetical prote
449	97	3.8	363	2	T19032	hypothetical prote
450	97	3.8	899	2	G02428	subtilisin-like pr
451	97	3.8	915	2	JC6148	subtilisin-like pr
452	97	3.8	1168	2	I56985	kalinin B1 - mouse
453	97	3.8	1184	2	A55184	fibulin-2 precurso
454	97	3.8	1436	2	A46496	antigen WC1.1 prec
455	97	3.8	2946	2	T15840	hypothetical prote
456	96.5	3.8	257	2	I50146	gene 17.5 protein
457	96.5	3.8	291	1	LNHU1	hepatic lectin H1
458	96.5	3.8	346	2	T46914	hypothetical prote
459	96.5	3.8	362	2	T19031	hypothetical prote
460	96.5	3.8	391	2	T34284	hypothetical prote
461	96.5	3.8	683	2	C36346	fibulin 1 precurso
462	96.5	3.8	1613	2	JE0272	low density lipopr
463	96	3.8	119	2	A34816	anticoagulant prot
464	96	3.8	237	2	JC7608	type II lectin-lik
465	96	3.8	942	2	D87803	protein bli-4D [im
466	96	3.8	1444	2	T18856	angiogenesis inhib
467	96	3.8	1786	1	MMMSB1	laminin beta-1 cha
468	96	3.8	4753	1	A47437	LDL-receptor-relat
469	95.5	3.8	144	2	PC7027	aggretin alpha cha
470	95.5	3.8	175	2	A41719	pancreatic stone p
471	95.5	3.8	363	2	T25278	hypothetical prote
472	95.5	3.8	371	1	JN0450	conglutinin precur
473	95.5	3.8	371	2	I45878	conglutinin - bovi
474	95.5	3.8	456	1	KXBO	protein C (activat
475	95.5	3.8	674	2	I55476	growth potentiatin
476	95.5	3.8	846	2	A30889	integrin beta chai
477	95.5	3.8	1049	1	S19421	ATP-dependent perm
478	95.5	3.8	1680	2	A43434	furin (EC 3.4.21.7
479	95.5	3.8	3020	2	A43932	mucin 2 precursor,
480	95	3.8	223	2	A35917	NK-cell receptor P
481	95	3.8	407	1	KFBO7	coagulation factor
482	95	3.8	408	2	T22801	hypothetical prote
483	95	3.8	419	2	S69207	vascular endotheli
484	95	3.8	889	1	VCLJG5	env polyprotein -
485	95	3.8	1603	2	T24098	hypothetical prote
486	94.5	3.7	136	2	JS0209	antistasin precurs
487	94.5	3.7	158	2	T26692	hypothetical prote
488	94.5	3.7	321	2	T19259	hypothetical prote
489	94.5	3.7	485	2	S36772	E-selectin - bovin
490	94.5	3.7	705	2	S34968	fibulin, splice fo
491	94.5	3.7	884	2	T18649	hypothetical prote
492	94	3.7	119	2	A86271	F21F23.19 protein
493	94	3.7	626	2	T04895	vacuolar sorting r
494	94	3.7	772	2	S32659	integrin beta 2 ch
495	94	3.7	1042	2	A57534	mucin 5AC (clone L
496	94	3.7	1170	2	A53612	laminin B1k chain
497	94	3.7	1506	2	T30886	integumentary muci
498	94	3.7	1786	1	MMHUB1	laminin beta-1 cha
499	93.5	3.7	81	2	A05264	pathogenesis-relat
500	93.5	3.7	131	2	JC5058	bitiscetin alpha c
501	93.5	3.7	175	2	S29822	pancreatitis-assoc
502	93.5	3.7	277	2	JC7903	collectin liver 1
503	93.5	3.7	461	1	KFHU	coagulation factor
504	93.5	3.7	589	2	C38128	epithelin/granulin
505	93.5	3.7	593	2	S45281	coagulation factor
506	93.5	3.7	880	1	VCLJS2	env polyprotein pr
507	93.5	3.7	1216	2	T26104	hypothetical prote
508	93.5	3.7	1613	2	JE0273	low density lipopr
509	93.5	3.7	2813	1	VWHU	von Willebrand fac
510	93.5	3.7	3507	2	T34513	hypothetical prote
511	93	3.7	216	2	PT0375	natural killer cel
512	93	3.7	232	2	T33704	hypothetical prote
513	93	3.7	343	2	S55369	follistatin - chic
514	93	3.7	361	2	G90738	probable dehydroge
515	93	3.7	361	2	A64817	malate dehydrogena
516	93	3.7	551	2	T16557	hypothetical prote
517	93	3.7	589	2	B38128	epithelin/granulin
518	93	3.7	685	2	S78040	fibulin, splice fo
519	93	3.7	768	2	A42755	P-selectin precurs
520	93	3.7	1192	2	S69000	laminin gamma 2 ch
521	92.5	3.7	129	2	JC4329	coagulation factor
522	92.5	3.7	147	2	JC7938	type II antifreeze
523	92.5	3.7	204	2	S27448	Sc7 protein - brac
524	92.5	3.7	221	2	T24494	hypothetical prote
525	92.5	3.7	368	2	T26338	hypothetical prote
526	92.5	3.7	411	2	D88087	protein B0454.7 [i
527	92.5	3.7	769	2	A41029	integrin beta-8 ch
528	92.5	3.7	1513	2	A54895	mucin 2, intestina
529	92	3.6	649	2	G86434	protein F17F8.23 [
530	92	3.6	881	2	S03068	env protein - huma
531	92	3.6	932	2	I52527	PACE4A - mouse (fr
532	92	3.6	2155	2	T30197	alpha tectorin - m
533	92	3.6	3375	2	T19821	hypothetical prote
534	91.5	3.6	160	2	JQ0542	185K secretory pro
535	91.5	3.6	205	2	T19851	hypothetical prote
536	91.5	3.6	247	1	LNRBPS	pulmonary surfacta
537	91.5	3.6	262	2	T34115	hypothetical prote
538	91.5	3.6	461	1	S18994	protein C (activat
539	91.5	3.6	596	2	A45664	variant-specific s
540	91	3.6	473	2	T32326	hypothetical prote

541	91	3.6	476	2	T27707	hypothetical prote
542	91	3.6	535	2	T32139	hypothetical prote
543	91	3.6	735	2	I48101	ADAM 6 protein pre
544	91	3.6	741	2	T46488	hypothetical prote
545	91	3.6	1162	2	T21557	hypothetical prote
546	91	3.6	3461	2	S58870	reelin precursor -
547	90.5	3.6	244	1	LNRTMC	mannose-binding le
548	90.5	3.6	308	2	T22393	hypothetical prote
549	90.5	3.6	405	2	S70150	tniQ protein - Xan
550	90.5	3.6	493	2	JC5621	epidermal growth f
551	90.5	3.6	621	2	I38467	low density lipopr
552	90.5	3.6	1104	2	I38869	transcription fact
553	90.5	3.6	1119	2	A88481	protein C16A3.6 [i
554	90.5	3.6	1170	2	A40558	thrombospondin 1 p
555	90.5	3.6	1250	2	T27706	hypothetical prote
556	90.5	3.6	1376	2	G00043	osteonidogen - hum
557	90.5	3.6	1548	2	S34583	serine proteinase
558	90	3.6	120	2	B28806	antistasin B - Mex
559	90	3.6	348	2	T28623	hypothetical prote
560	90	3.6	349	2	D36858	gene G4R protein -
561	90	3.6	349	2	D72175	G2R protein - vari
562	90	3.6	365	2	PQ0839	envelope protein -
563	90	3.6	550	2	I37579	DiGeorge syndrome
564	90	3.6	646	2	H96665	protein F22C12.10
565	90	3.6	863	1	S51789	VLDL receptor prec
566	90	3.6	886	2	T11555	env protein - simi
567	90	3.6	937	2	I53282	gene PACE4 protein
568	90	3.6	1106	2	T44598	hypothetical prote
569	90	3.6	1106	2	T13938	gene shuttle craft
570	90	3.6	1265	2	S57968	Ran-binding protei
571	90	3.6	1642	2	T19130	hypothetical prote
572	90	3.6	2090	2	T30075	hypothetical prote
573	89.5	3.5	199	2	JH0822	lymphocyte early a
574	89.5	3.5	212	2	T20581	hypothetical prote
575	89.5	3.5	420	2	A88962	protein F59A7.1 [i
576	89.5	3.5	572	2	T29880	hypothetical prote
577	89.5	3.5	601	2	B36346	fibulin 1 precurso
578	89.5	3.5	675	1	KXMSS	plasma protein S p
579	89.5	3.5	713	2	A35502	major surface-labe
580	89.5	3.5	736	2	T19366	hypothetical prote
581	89.5	3.5	925	2	T37475	lipoprotein recept
582	89.5	3.5	1023	2	T30257	IgG Fc binding pro
583	89.5	3.5	1234	1	NBMSH	complement factor
584	89.5	3.5	1327	2	D70759	probable otsB prot
585	89.5	3.5	1712	2	A38261	masking protein pr
586	89	3.5	361	2	A85589	probable dehydroge
587	89	3.5	405	2	T23099	hypothetical prote
588	89	3.5	676	2	B47222	Kallmann syndrome
589	89	3.5	746	2	G02838	enhancer-of-zeste
590	89	3.5	918	2	JC4361	scavenger receptor
591	89	3.5	928	2	T01191	RNA-directed DNA p
592	89	3.5	1339	2	JC4387	epidermal growth f
593	89	3.5	1342	2	A36223	kinase-related tra
594	89	3.5	1558	2	C89114	protein C37C3.6a [
595	89	3.5	1984	2	T13171	probable vitelloge
596	89	3.5	2153	2	T30074	hypothetical prote
597	89	3.5	2167	2	T34395	hypothetical prote
598	89	3.5	3133	2	S52093	hemocytin - silkwo
599	89	3.5	5147	1	IJFFTM	cadherin-related t
600	88.5	3.5	152	2	JC7134	agkisacutacin alph
601	88.5	3.5	257	2	T18969	hypothetical prote
602	88.5	3.5	376	2	JC4892	L-selectin precurs
603	88.5	3.5	459	2	JQ0419	coagulation factor
604	88.5	3.5	482	1	EXRT	coagulation factor
605	88.5	3.5	492	2	T21934	hypothetical prote
606	88.5	3.5	557	2	A48434	variant-specific s
607	88.5	3.5	646	2	JN0473	P-selectin precurs
608	88.5	3.5	746	2	S44792	F09G8.8 protein -
609	88.5	3.5	769	1	JC1121	leukocyte adhesion
610	88.5	3.5	981	2	S51604	receptor-like tyro
611	88.5	3.5	1005	2	S49015	receptor tyrosine
612	88.5	3.5	1170	1	TSHUP1	thrombospondin 1 p
613	88.5	3.5	1189	2	AH2154	WD-repeat protein
614	88.5	3.5	2403	2	A59386	sanko - human
615	88	3.5	224	2	T33202	hypothetical prote
616	88	3.5	262	2	T24854	hypothetical prote
617	88	3.5	667	2	A48579	trophozoite surfac
618	88	3.5	798	2	A28193	integrin beta-1 ch
619	88	3.5	823	2	S18968	cyritestin precurs
620	88	3.5	2395	1	S50820	surface protein ty
621	88	3.5	2533	2	T28674	alpha-51D-immobili
622	87.5	3.5	152	2	JC4690	coagulation factor
623	87.5	3.5	333	2	T21595	hypothetical prote
624	87.5	3.5	356	2	A25918	thrombomodulin - b
625	87.5	3.5	455	2	A55050	enigma - human
626	87.5	3.5	1308	2	A47253	epidermal growth f
627	87.5	3.5	1959	1	AGRT	agrin - rat
628	87.5	3.5	2543	2	T31687	suface antigen - P
629	87.5	3.5	3051	2	S42373	hypothetical prote
630	87.5	3.5	4660	2	T42737	gp330 protein prec
631	87.5	3.5	13288	2	T03099	mucin, submaxillar
632	87	3.4	170	2	T23772	hypothetical prote
633	87	3.4	248	1	LNHUMC	mannose-binding le
634	87	3.4	253	2	T25768	hypothetical prote
635	87	3.4	365	2	PQ0838	envelope protein -
636	87	3.4	365	2	PQ0840	envelope protein -
637	87	3.4	558	2	T17324	hypothetical prote
638	87	3.4	594	2	T04783	hypothetical prote
639	87	3.4	798	2	B28193	integrin beta-1* c
640	87	3.4	869	1	JC4858	VLDL receptor prec
641	87	3.4	1584	2	T22674	hypothetical prote
642	87	3.4	1715	2	C40228	neurexin II-alpha
643	86.5	3.4	233	2	T25295	hypothetical prote
644	86.5	3.4	238	1	LNRTMA	mannose-binding le
645	86.5	3.4	302	2	B71310	conserved hypothet
646	86.5	3.4	324	2	T25019	hypothetical prote
647	86.5	3.4	623	2	T06794	vacuolar sorting r
648	86.5	3.4	794	2	F88508	protein H14A12.6 [
649	86.5	3.4	1019	2	A38738	coagulation factor
650	86.5	3.4	1743	2	T26859	hypothetical prote
651	86.5	3.4	2120	2	T30243	alpha tectorin - c
652	86.5	3.4	2477	2	S14428	fibronectin precur
653	86	3.4	120	2	A28806	antistasin A - Mex
654	86	3.4	294	2	T23682	hypothetical prote
655	86	3.4	363	2	JE0111	lectin-like oxidiz
656	86	3.4	413	2	T23098	hypothetical prote
657	86	3.4	427	2	S74211	PAS-6/7 protein pr
658	86	3.4	482	2	JC5092	E-selectin - pig
659	86	3.4	533	2	T33912	hypothetical prote
660	86	3.4	586	1	QRXLE	estrogen receptor
661	86	3.4	624	2	T00044	vacuolar sorting r
662	86	3.4	816	2	C69493	hypothetical prote
663	86	3.4	995	2	A56599	embryo kinase 5 -
664	86	3.4	1063	1	GNWVR4	structural polypro
665	86	3.4	1394	2	A35626	transforming growt
666	85.5	3.4	175	2	A49616	pancreatitis-assoc
667	85.5	3.4	380	2	G01639	transmembrane prot
668	85.5	3.4	382	2	T25280	hypothetical prote
669	85.5	3.4	402	2	S42367	lag-2 protein - Ca
670	85.5	3.4	446	2	T31644	hypothetical prote
671	85.5	3.4	451	2	T23265	hypothetical prote
672	85.5	3.4	502	2	T20130	hypothetical prote
673	85.5	3.4	531	2	T22021	hypothetical prote
674	85.5	3.4	605	2	S71630	metalloproteinase
675	85.5	3.4	626	1	NDBE61	exonuclease (EC 3.
676	85.5	3.4	646	2	S38819	plasma protein S -
677	85.5	3.4	803	2	F83360	glucose dehydrogen
678	85.5	3.4	838	2	T20125	hypothetical prote
679	85.5	3.4	991	2	I78843	receptor protein-t
680	85.5	3.4	1019	2	T13039	tyrosine kinase re
681	85.5	3.4	1251	2	A57293	latent transformin
682	85.5	3.4	1847	2	T18308	probable vitelloge
683	85.5	3.4	2153	2	T14893	scavenger receptor
684	85.5	3.4	2219	2	T27684	hypothetical prote
685	85.5	3.4	2265	1	FNBO	fibronectin - bovi
686	85.5	3.4	3097	2	T00021	DN-cadherin - frui

687	85	3.4	119	2	A34398	antistasin - Mexic
688	85	3.4	119	2	S13904	antistasin - Mexic
689	85	3.4	188	2	T33623	hypothetical prote
690	85	3.4	223	2	B38346	ultra-high-sulfur
691	85	3.4	334	2	T20524	hypothetical prote
692	85	3.4	483	2	G64799	ybeV protein - Esc
693	85	3.4	732	2	I52361	testicular metallo
694	85	3.4	768	2	I53821	P-selectin - rat
695	85	3.4	815	2	H82137	biotin sulfoxide r
696	85	3.4	826	2	A60385	monocyte surface a
697	85	3.4	956	2	A57121	thrombospondin 3 p
698	85	3.4	1265	1	A37967	neural cell adhesi
699	85	3.4	1955	1	AGCH	agrin precursor -
700	84.5	3.3	171	2	I49612	teratocarcinoma-de
701	84.5	3.3	227	1	S68150	eosinophil major b
702	84.5	3.3	227	2	D83451	hypothetical prote
703	84.5	3.3	239	1	LNMSMA	mannose-binding le
704	84.5	3.3	411	2	A84365	hypothetical prote
705	84.5	3.3	416	2	T20448	hypothetical prote
706	84.5	3.3	422	1	KXHUZ	plasma protein Z p
707	84.5	3.3	676	1	KXHUS	plasma protein S p
708	84.5	3.3	700	2	A96690	hypothetical prote
709	84.5	3.3	828	2	T22367	hypothetical prote
710	84.5	3.3	837	2	A42112	mucin-like peptide
711	84.5	3.3	1650	2	S53457	dominant autoantig
712	84.5	3.3	1713	2	A55347	adhesive ligand ep
713	84	3.3	133	2	A47267	botrocetin alpha c
714	84	3.3	372	2	S23936	L-selectin precurs
715	84	3.3	464	2	T32401	hypothetical prote
716	84	3.3	491	2	JC6197	stromelysin 3 (EC
717	84	3.3	497	2	T33013	hypothetical prote
718	84	3.3	688	2	H91029	probable peptidase
719	84	3.3	688	2	A85874	probable peptidase
720	84	3.3	830	2	A30359	P-selectin precurs
721	84	3.3	1178	1	A39804	thrombospondin pre
722	84	3.3	1766	2	A42125	trophozoite cystei
723	83.5	3.3	175	1	JH0626	antifreeze protein
724	83.5	3.3	175	2	A37194	pancreatic thread
725	83.5	3.3	230	2	A38346	ultra-high-sulfur
726	83.5	3.3	248	2	A48853	pulmonary surfacta
727	83.5	3.3	321	2	T26153	hypothetical prote
728	83.5	3.3	439	2	T16493	hypothetical prote
729	83.5	3.3	452	1	A30351	coagulation factor
730	83.5	3.3	558	2	JC5878	plasma hyaluronan-
731	83.5	3.3	642	2	S53434	plasma protein S p
732	83.5	3.3	647	2	S75116	squalene-hopene-cy
733	83.5	3.3	700	2	T32205	hypothetical prote
734	83.5	3.3	736	2	S47645	tMDC I protein - c
735	83.5	3.3	736	2	T06757	hypothetical prote
736	83.5	3.3	858	1	VCLJG2	env polyprotein pr
737	83.5	3.3	915	2	B48225	probable proprotei
738	83.5	3.3	987	2	I48652	mouse developmenta
739	83.5	3.3	987	2	I48953	eph-related recept
740	83.5	3.3	1013	2	I50615	receptor-type prot
741	83.5	3.3	2733	2	S15760	genome polyprotein
742	83.5	3.3	4351	2	T00252	MEGF1 protein - ra
743	83	3.3	174	2	S54979	pancreatitis-assoc
744	83	3.3	174	2	G88102	protein W10G11.12
745	83	3.3	178	2	JC1467	betacellulin precu
746	83	3.3	188	2	A39787	teratocarcinoma-de
747	83	3.3	211	2	A46458	human CR1 homolog
748	83	3.3	225	2	I38700	hNKR-P1a protein -
749	83	3.3	401	2	S65138	glycoprotein antig
750	83	3.3	423	2	S11974	polyketide beta-ke
751	83	3.3	524	2	JC7980	metalloprotease-re
752	83	3.3	814	2	G02390	disintegrin-like m
753	83	3.3	1034	2	JC5598	mucin - rat
754	83	3.3	1166	1	S06142	protein-tyrosine k
755	83	3.3	1213	2	D86384	unknown protein [i
756	83	3.3	1296	2	T16859	hypothetical prote
757	83	3.3	1615	2	JE0372	low density lipopr
758	82.5	3.3	179	2	T22471	hypothetical prote
759	82.5	3.3	212	2	T24999	hypothetical prote
760	82.5	3.3	241	2	T16802	hypothetical prote
761	82.5	3.3	248	1	LNRTPS	pulmonary surfacta
762	82.5	3.3	295	2	JC5559	lectin-B - Virgini
763	82.5	3.3	372	2	A55262	protein kinase (EC
764	82.5	3.3	421	2	T25383	hypothetical prote
765	82.5	3.3	591	2	I48141	acrogranin - guine
766	82.5	3.3	610	2	T16761	hypothetical prote
767	82.5	3.3	670	2	I65967	disintegrin-like m
768	82.5	3.3	734	2	JC4861	fertillin beta cha
769	82.5	3.3	755	2	A44315	cartilage oligomer
770	82.5	3.3	775	2	T21436	hypothetical prote
771	82.5	3.3	780	2	A34102	von Willebrand fac
772	82.5	3.3	791	2	T42691	hypothetical prote
773	82.5	3.3	915	1	A48225	subtilisin-like pr
774	82.5	3.3	1042	2	T26644	hypothetical prote
775	82.5	3.3	1780	2	T20695	hypothetical prote
776	82.5	3.3	2205	1	MNWVRN	nonstructural poly
777	82.5	3.3	2533	2	T28675	alpha-51D immobili
778	82.5	3.3	2769	1	UIBO	thyroglobulin prec
779	82	3.2	155	2	T24840	hypothetical prote
780	82	3.2	186	2	A28401	agglutinin isolect
781	82	3.2	212	2	T05936	agglutinin isolect
782	82	3.2	212	2	S09623	agglutinin isolect
783	82	3.2	290	2	T21868	hypothetical prote
784	82	3.2	319	2	A53502	follistatin - Afri
785	82	3.2	417	2	T29864	hypothetical prote
786	82	3.2	437	2	S05478	properdin - mouse
787	82	3.2	477	2	JS0597	t-plasminogen acti
788	82	3.2	643	2	T25473	hypothetical prote
789	82	3.2	650	2	A34498	glycoprotein antig
790	82	3.2	688	2	B65005	hypothetical prote
791	82	3.2	843	2	A27131	epidermal growth f
792	82	3.2	909	1	QRXLL2	LDL receptor 2 pre
793	82	3.2	956	1	A46016	thrombospondin 3 -
794	82	3.2	1063	1	GNWVRA	structural polypro
795	82	3.2	1245	1	VHWV82	structural polypro
796	82	3.2	1328	2	T43060	agrin - electric r
797	81.5	3.2	228	2	T22394	hypothetical prote
798	81.5	3.2	357	2	S23403	sperm surface prot
799	81.5	3.2	371	2	F83487	hypothetical prote
800	81.5	3.2	376	2	S70841	hypothetical trans
801	81.5	3.2	446	2	I25797	NADH2 dehydrogenas
802	81.5	3.2	456	2	T17887	lysine/proline-ric
803	81.5	3.2	471	2	E83173	hypothetical prote
804	81.5	3.2	491	2	T21421	hypothetical prote
805	81.5	3.2	625	1	KFHU1	coagulation factor
806	81.5	3.2	703	2	T04191	hypothetical prote
807	81.5	3.2	738	2	T27789	hypothetical prote
808	81.5	3.2	957	2	T15976	hypothetical prote
809	81.5	3.2	962	2	JC5571	subtilisin-like pr
810	81.5	3.2	969	1	A39490	subtilisin-like pr
811	81.5	3.2	975	2	JC5570	subtilisin-like pr
812	81.5	3.2	1063	1	GNWV77	structural polypro
813	81.5	3.2	1172	1	TSHUP2	thrombospondin 2 p
814	81.5	3.2	1217	1	EGMSMG	epidermal growth f
815	81.5	3.2	1268	2	B36502	insulin receptor-r
816	81.5	3.2	2165	2	T21371	hypothetical prote
817	81.5	3.2	2215	2	T00348	LR11 protein - mou
818	81	3.2	260	2	F95899	probable transcrip
819	81	3.2	274	2	H70900	hypothetical prote
820	81	3.2	282	1	YPDOD1	prestalk D11 prote
821	81	3.2	405	2	G70829	probable molybdenu
822	81	3.2	409	2	T29517	hypothetical prote
823	81	3.2	416	1	KFBO	coagulation factor
824	81	3.2	455	2	T42670	hypothetical prote
825	81	3.2	492	1	EXBO	coagulation factor
826	81	3.2	529	2	S51477	extracellular glyc
827	81	3.2	560	1	JC4795	plasma hyaluronan-
828	81	3.2	575	2	T34280	hypothetical prote
829	81	3.2	610	2	JC7315	myoneurin - human
830	81	3.2	674	2	A47222	Kallmann syndrome
831	81	3.2	704	2	B84685	hypothetical prote
832	81	3.2	761	2	JC5759	brain-specific ser

833	81	3.2	869	2	A47665	env protein gp120(
834	81	3.2	1077	2	T41146	probable cysteine-
835	81	3.2	1599	2	T16210	hypothetical prote
836	81	3.2	2767	1	UIHU	thyroglobulin prec
837	80.5	3.2	168	2	B88102	protein W09G10.5 [
838	80.5	3.2	233	1	S13625	eosinophil major b
839	80.5	3.2	245	2	S43565	R01H10.4 protein (
840	80.5	3.2	289	2	T25682	hypothetical prote
841	80.5	3.2	471	1	S08325	flavonol 3-O-gluco
842	80.5	3.2	471	2	S01052	flavonol 3-O-gluco
843	80.5	3.2	558	2	E91170	hypothetical prote
844	80.5	3.2	558	2	E86016	probable enzyme Z4
845	80.5	3.2	597	2	S71352	metalloproteinase
846	80.5	3.2	612	2	JH0799	laminin-related pr
847	80.5	3.2	1133	1	EGRT	epidermal growth f
848	80.5	3.2	1255	1	A24571	protein-tyrosine k
849	80.5	3.2	2731	1	VFIHJH	genome polyprotein
850	80	3.2	208	2	T29676	hypothetical prote
851	80	3.2	245	2	AB0788	heme exporter prot
852	80	3.2	248	2	AE0960	heme exporter prot
853	80	3.2	284	2	T25938	hypothetical prote
854	80	3.2	353	2	T44500	fls485 protein [im
855	80	3.2	359	2	T22731	hypothetical prote
856	80	3.2	428	2	T07814	S-locus-specific g
857	80	3.2	449	2	F75558	hypothetical prote
858	80	3.2	477	1	A34369	t-plasminogen acti
859	80	3.2	477	2	JS0598	t-plasminogen acti
860	80	3.2	494	2	T14516	S-locus-specific g
861	80	3.2	537	2	JC6182	isocitrate lyase (
862	80	3.2	585	2	B49596	genome polyprotein
863	80	3.2	699	2	T33375	hypothetical prote
864	80	3.2	713	2	I65253	disintegrin-like t
865	80	3.2	787	2	A55034	6-phosphofructokin
866	80	3.2	875	2	T20429	hypothetical prote
867	80	3.2	1016	2	T05066	hypothetical prote
868	80	3.2	1264	2	T19545	hypothetical prote
869	80	3.2	1708	2	AE1866	WD-40 repeat prote
870	80	3.2	5149	2	F83345	probable non-ribos
871	79.5	3.1	146	2	JC4691	coagulation factor
872	79.5	3.1	320	2	A53119	cell adhesion glyc
873	79.5	3.1	379	2	G75357	diaminopimelate de
874	79.5	3.1	480	2	E88656	protein F56D6.2 [i
875	79.5	3.1	618	2	T00476	probable vacuolar
876	79.5	3.1	770	2	D89447	protein F57C12.1 [
877	79.5	3.1	854	1	QRHYLD	LDL receptor precu
878	79.5	3.1	1006	2	JC5526	kinase-defective E
879	79.5	3.1	1217	2	T22672	hypothetical prote
880	79.5	3.1	1357	2	T16860	hypothetical prote
881	79.5	3.1	1634	1	JC5500	phosphoinositide 3
882	79	3.1	169	1	S18946	ultra high-sulfur
883	79	3.1	188	2	A30362	teratocarcinoma-de
884	79	3.1	248	2	T19913	hypothetical prote
885	79	3.1	325	2	S68985	exogastrula-induci
886	79	3.1	335	2	A70851	probable trxB2 pro
887	79	3.1	370	2	S22124	L-selectin precurs
888	79	3.1	466	1	NMIV4	exo-alpha-sialidas
889	79	3.1	466	1	KFHU7	coagulation factor
890	79	3.1	482	2	AC0426	serine-type D-Ala-
891	79	3.1	511	2	T17298	hypothetical prote
892	79	3.1	524	2	S38539	disintegrin-like m
893	79	3.1	582	2	B45878	hypothetical prote
894	79	3.1	695	2	B75295	hypothetical prote
895	79	3.1	725	2	S13426	multidrug resistan
896	79	3.1	735	2	G02937	fertilin beta - cr
897	79	3.1	751	2	F87789	protein C34G6.2 [i
898	79	3.1	984	1	A34076	protein-tyrosine k
899	79	3.1	1245	1	VHWVB	structural polypro
900	79	3.1	1607	2	T43212	insulin-like growt
901	78.5	3.1	213	1	AEWT2	agglutinin isolect
902	78.5	3.1	249	2	T31837	hypothetical prote
903	78.5	3.1	344	2	I57698	follistatin - rat
904	78.5	3.1	384	2	S76402	hypothetical prote
905	78.5	3.1	475	2	T35697	arabinofuranosidas
906	78.5	3.1	546	2	T49931	hypothetical prote
907	78.5	3.1	831	2	T25827	hypothetical prote
908	78.5	3.1	850	2	S56015	gastric mucin MUC5
909	78.5	3.1	1046	2	A26838	prestalk protein p
910	78.5	3.1	1051	2	T48933	WD repeat domain p
911	78.5	3.1	1172	2	A42587	thrombospondin 2 p
912	78.5	3.1	1300	2	A36502	insulin receptor-r
913	78.5	3.1	1363	1	VGIHQU	E2 glycoprotein pr
914	78.5	3.1	1363	1	VGIHF1	E2 glycoprotein pr
915	78.5	3.1	2241	2	T02857	conserved hypothet
916	78	3.1	170	2	T28140	natural killer cel
917	78	3.1	213	2	T27841	hypothetical prote
918	78	3.1	221	2	T17997	hypothetical prote
919	78	3.1	244	1	LNMSMC	mannose-binding le
920	78	3.1	372	1	A32375	L-selectin precurs
921	78	3.1	443	2	I46932	coagulation factor
922	78	3.1	472	2	E87658	NAD(P) transhydrog
923	78	3.1	625	2	F84706	probable vacuolar
924	78	3.1	689	2	T52060	protein MEDEA [imp
925	78	3.1	864	2	T48474	hypothetical prote
926	78	3.1	1027	2	T19173	hypothetical prote
927	78	3.1	1067	2	D75625	probable extracell
928	78	3.1	2594	2	A35774	kinase-related pro
929	77.5	3.1	172	2	I47106	high-sulfur wool m
930	77.5	3.1	190	2	T26566	hypothetical prote
931	77.5	3.1	227	1	LNRZ	lectin precursor -
932	77.5	3.1	281	2	D88637	protein W09G12.1 [
933	77.5	3.1	325	2	B43692	T2 protein - rabbi
934	77.5	3.1	344	1	A27701	follistatin precur
935	77.5	3.1	344	2	A32141	follistatin i prec
936	77.5	3.1	347	2	T20618	hypothetical prote
937	77.5	3.1	383	2	F83321	hypothetical prote
938	77.5	3.1	391	2	T36311	probable lipase -
939	77.5	3.1	415	2	T20335	hypothetical prote
940	77.5	3.1	491	2	S52920	disintegrin (EC 3.
941	77.5	3.1	639	2	T33166	hypothetical prote
942	77.5	3.1	675	1	KXRTS	plasma protein S p
943	77.5	3.1	701	2	S61239	hypothetical prote
944	77.5	3.1	879	1	QRRTLD	LDL receptor precu
945	77.5	3.1	992	1	GNWVR3	structural polypro
946	77.5	3.1	998	2	I58351	receptor protein-t
947	77.5	3.1	1160	2	F88369	protein unc-52 [im
948	77.5	3.1	2295	2	C88369	protein unc-52 [im
949	77	3.0	156	2	T28141	C type lectin, B l
950	77	3.0	222	1	JL0085	eosinophil major b
951	77	3.0	230	2	T31722	hypothetical prote
952	77	3.0	240	2	T20657	hypothetical prote
953	77	3.0	250	1	A49053	CD27 antigen precu
954	77	3.0	284	2	G75447	hypothetical prote
955	77	3.0	289	2	AE0660	probable oxidoredu
956	77	3.0	357	2	C42087	a2-pheromone recep
957	77	3.0	359	2	G86290	hypothetical prote
958	77	3.0	403	2	T27948	hypothetical prote
959	77	3.0	428	2	T14530	S-locus-specific g
960	77	3.0	461	2	T00621	hypothetical prote
961	77	3.0	470	2	A40697	63K sperm flagella
962	77	3.0	474	2	A57480	tubulointerstitial
963	77	3.0	677	2	C42125	trophozoite cystei
964	77	3.0	680	2	S17982	Kallmann syndrome
965	77	3.0	741	2	A83271	hypothetical prote
966	77	3.0	751	2	AI3392	phosphoribosylform
967	77	3.0	850	2	JC5700	ErbB kinase activa
968	77	3.0	873	1	A49729	VLDL receptor prec
969	77	3.0	883	2	T49781	related to mutanas
970	77	3.0	886	2	A57172	probable hormone r
971	77	3.0	1223	1	TVCHLV	epidermal growth f
972	77	3.0	1245	1	MMMSND	nidogen precursor
973	77	3.0	1309	2	T00078	probable RNA-direc
974	77	3.0	1784	2	T10532	gag-pol polyprotei
975	77	3.0	2233	2	T28669	surface protein 51
976	76.5	3.0	179	2	T25841	hypothetical prote
977	76.5	3.0	208	1	JC1409	heparin-binding EG
978	76.5	3.0	229	2	T34325	hypothetical prote

979	76.5	3.0	245	2	T19586	hypothetical prote
980	76.5	3.0	258	2	T10083	expansin S2 precur
981	76.5	3.0	317	2	T25279	hypothetical prote
982	76.5	3.0	318	2	T20063	hypothetical prote
983	76.5	3.0	328	2	G89152	protein C24B5.5 [i
984	76.5	3.0	389	2	AH2931	conserved hypothet
985	76.5	3.0	417	2	T33376	hypothetical prote
986	76.5	3.0	425	2	F98350	hypothetical prote
987	76.5	3.0	433	2	S58087	estrogen receptor
988	76.5	3.0	471	2	S01037	flavonol 3-O-gluco
989	76.5	3.0	497	2	T27827	hypothetical prote
990	76.5	3.0	605	2	T33913	hypothetical prote
991	76.5	3.0	621	2	G31844	tra protein - Stre
992	76.5	3.0	638	2	T41478	probable transcrip
993	76.5	3.0	836	2	AB0540	outer-membrane fim
994	76.5	3.0	893	2	S51603	receptor-like tyro
995	76.5	3.0	1059	2	T22545	hypothetical prote
996	76.5	3.0	1474	2	D88550	protein ZC84.6 [im
997	76.5	3.0	1965	2	T33216	hypothetical prote
998	76.5	3.0	2844	2	S28291	hypothetical prote
999	76	3.0	212	2	T22463	hypothetical prote
1000	76	3.0	239	2	S07406	thaumatin homolog
1001	76	3.0	266	2	I49050	Ly-49E-GE antigen
1002	76	3.0	289	2	T25277	hypothetical prote
1003	76	3.0	289	2	S23402	sperm surface prot
1004	76	3.0	305	2	T02851	probable membrane
1005	76	3.0	328	2	T16970	GTP-binding protei
1006	76	3.0	335	2	A39743	u-plasminogen acti
1007	76	3.0	370	2	T22082	hypothetical prote
1008	76	3.0	372	2	T31060	hypothetical prote
1009	76	3.0	385	2	T26487	hypothetical prote
1010	76	3.0	581	2	B54665	netrin-2 precursor
1011	76	3.0	688	2	T27020	hypothetical prote
1012	76	3.0	699	2	T09483	Cys-rich protein R
1013	76	3.0	996	2	JE0237	apolipoprotein E r
1014	76	3.0	1107	2	T15884	hypothetical prote
1015	76	3.0	1142	2	T30272	hypothetical prote
1016	76	3.0	1247	1	MMHUND	nidogen precursor
1017	76	3.0	1297	2	T30274	proteoliaisin - se
1018	76	3.0	1518	2	T28880	hypothetical prote
1019	76	3.0	1627	2	S65464	pregnancy-associat
1020	76	3.0	1666	2	T38393	clathrin heavy cha
1021	76	3.0	2083	2	T42721	CRP-ductin-alpha p
1022	76	3.0	2115	2	S38480	nonstructural prot
1023	75.5	3.0	130	2	C88102	protein W09G10.6 [
1024	75.5	3.0	195	2	T28803	hypothetical prote
1025	75.5	3.0	197	2	I46413	keratin KAP5.5 - s
1026	75.5	3.0	252	2	G75485	hypothetical prote
1027	75.5	3.0	255	2	T03299	expansin 3 - rice
1028	75.5	3.0	290	2	T21185	hypothetical prote
1029	75.5	3.0	323	1	S09702	L-selectin precurs
1030	75.5	3.0	331	2	B70837	hypothetical prote
1031	75.5	3.0	338	2	T18715	hypothetical prote
1032	75.5	3.0	371	2	T08485	klcB protein - Ent
1033	75.5	3.0	385	1	A34015	L-selectin precurs
1034	75.5	3.0	423	2	B70931	probable PPE prote
1035	75.5	3.0	431	2	JS0599	t-plasminogen acti
1036	75.5	3.0	436	2	T07816	S-locus-specific g
1037	75.5	3.0	446	2	S01187	NADH2 dehydrogenas
1038	75.5	3.0	461	1	GQRTT1	tumor necrosis fac
1039	75.5	3.0	493	2	S32037	finger protein XFG
1040	75.5	3.0	499	2	B56021	probable cell divi
1041	75.5	3.0	508	2	T26636	hypothetical prote
1042	75.5	3.0	523	2	F71302	asparagine-tRNA li
1043	75.5	3.0	603	1	GBECGC	beta-glucuronidase
1044	75.5	3.0	605	2	JC5673	receptor tyrosine
1045	75.5	3.0	610	2	I48612	developmental kina
1046	75.5	3.0	626	2	T27319	hypothetical prote
1047	75.5	3.0	626	2	I48614	developmental kina
1048	75.5	3.0	655	2	JC7850	disintegrin and me
1049	75.5	3.0	729	2	T41735	probable n-termina
1050	75.5	3.0	822	2	S70012	methionine-S-oxide
1051	75.5	3.0	860	2	T16892	hypothetical prote
1052	75.5	3.0	885	2	S04322	env polyprotein -
1053	75.5	3.0	898	2	S47489	receptor tyrosine
1054	75.5	3.0	987	2	A54092	protein-tyrosine k
1055	75.5	3.0	998	2	JC5672	receptor tyrosine
1056	75.5	3.0	1115	2	S40241	G protein-coupled
1057	75.5	3.0	1205	2	T18517	procollagen N-endo
1058	75.5	3.0	1207	1	EGHU	epidermal growth f
1059	75.5	3.0	1280	2	A39117	170K lectin precur
1060	75.5	3.0	1293	1	A46350	RNA-directed RNA p
1061	75.5	3.0	1717	1	A45558	epidermal growth f
1062	75.5	3.0	5825	2	T12117	polyprotein - fava
1063	75	3.0	266	2	I36855	gene B9R protein -
1064	75	3.0	267	2	G65103	pts system, n-acet
1065	75	3.0	287	2	AI2609	regulator protein
1066	75	3.0	287	2	H97391	probable regulator
1067	75	3.0	330	2	T25169	hypothetical prote
1068	75	3.0	343	2	S45321	follistatin - mous
1069	75	3.0	345	2	T22399	hypothetical prote
1070	75	3.0	346	2	H90849	hypothetical prote
1071	75	3.0	346	2	G85707	unknown protein en
1072	75	3.0	429	2	B87039	conserved hypothet
1073	75	3.0	458	1	S77662	thioredoxin-disulf
1074	75	3.0	492	2	A44399	stromelysin 3 (EC
1075	75	3.0	507	2	S36484	L1 protein - human
1076	75	3.0	603	1	VCFVER	env polyprotein -
1077	75	3.0	629	2	S73172	DNA-directed RNA p
1078	75	3.0	661	2	B96596	hypothetical prote
1079	75	3.0	764	2	C86314	hypothetical prote
1080	75	3.0	870	2	T31795	hypothetical prote
1081	75	3.0	972	2	A30363	glycoprotein GP330
1082	75	3.0	980	2	S71090	peroxisome biogene
1083	75	3.0	1056	2	A53767	mucin MUC5B, trach
1084	75	3.0	1239	2	I49705	glutamate receptor
1085	75	3.0	1274	2	T42017	cysteine rich prot
1086	75	3.0	1379	2	T45119	FIM protein [impor
1087	75	3.0	1443	2	G75393	hypothetical prote
1088	75	3.0	4957	2	T03455	ALR protein - huma
1089	75	3.0	5262	2	T03454	ALR protein - huma
1090	74.5	2.9	149	2	T27305	hypothetical prote
1091	74.5	2.9	189	2	T27837	hypothetical prote
1092	74.5	2.9	233	2	G83462	heme exporter prot
1093	74.5	2.9	250	2	T31835	hypothetical prote
1094	74.5	2.9	296	2	D88969	protein F15E11.9 [
1095	74.5	2.9	344	2	I45894	follistatin - bovi
1096	74.5	2.9	400	2	AF2107	hypothetical prote
1097	74.5	2.9	405	2	B36340	alpha(1,3)-fucosyl
1098	74.5	2.9	417	2	T08724	hypothetical prote
1099	74.5	2.9	465	2	T05734	glutamyl-tRNA redu
1100	74.5	2.9	506	2	S57663	cellulase (EC 3.2.
1101	74.5	2.9	550	1	VGIHD6	E2 glycoprotein pr
1102	74.5	2.9	747	2	T06580	subtilisin-like pr
1103	74.5	2.9	754	2	AE0614	probable competenc
1104	74.5	2.9	881	1	VCLJG3	env polyprotein -
1105	74.5	2.9	1049	2	C95883	probable efflux pr
1106	74.5	2.9	1206	1	VGVURV	M polyprotein - Ri
1107	74.5	2.9	1360	2	T33922	hypothetical prote
1108	74.5	2.9	1363	1	VGIHNM	E2 glycoprotein pr
1109	74.5	2.9	1428	2	T08852	lustrin A - Califo
1110	74.5	2.9	2396	2	B36861	orf 1a protein - L
1111	74.5	2.9	3161	2	T30342	protein HMWP1 - Ye
1112	74	2.9	171	2	T44537	hypothetical prote
1113	74	2.9	249	2	T17878	hypothetical prote
1114	74	2.9	254	2	T20779	hypothetical prote
1115	74	2.9	258	2	A81950	hypothetical prote
1116	74	2.9	264	2	AE0096	thymidylate syntha
1117	74	2.9	274	2	C85084	hypothetical prote
1118	74	2.9	317	2	B86415	peroxisomal target
1119	74	2.9	337	2	I47079	follistatin - shee
1120	74	2.9	347	2	T22395	hypothetical prote
1121	74	2.9	372	2	A83260	hypothetical prote
1122	74	2.9	410	2	C64831	ycaQ protein - Esc
1123	74	2.9	457	2	C86464	hypothetical prote
1124	74	2.9	479	2	S72582	hypothetical prote

1125	74	2.9	502	2	T01378	nicotinic receptor
1126	74	2.9	550	2	T47158	hypothetical prote
1127	74	2.9	571	2	A81797	hypothetical prote
1128	74	2.9	600	2	S07638	spore coat protein
1129	74	2.9	604	2	AC1083	toxin components h
1130	74	2.9	623	2	T47542	Spot 3 protein and
1131	74	2.9	695	2	S49163	transferrin precur
1132	74	2.9	791	2	A53691	diacylglycerol kin
1133	74	2.9	796	1	JC1285	protein-tyrosine-p
1134	74	2.9	801	2	A47744	diacylglycerol kin
1135	74	2.9	855	2	A45713	Env transmembrane
1136	74	2.9	862	1	QRMSLD	LDL receptor precu
1137	74	2.9	880	2	T19076	hypothetical prote
1138	74	2.9	1029	2	A87349	hypothetical prote
1139	74	2.9	1250	1	B45219	N-methyl-D-asparta
1140	74	2.9	1364	2	T51920	probable xanthine
1141	74	2.9	2588	2	T14342	NSD1 protein - mou
1142	74	2.9	3069	2	H70656	fatty-acid synthas
1143	73.5	2.9	176	2	T31796	hypothetical prote
1144	73.5	2.9	245	2	H91014	heme exporter prot
1145	73.5	2.9	245	2	B85859	heme exporter prot
1146	73.5	2.9	245	2	E64989	heme exporter prot
1147	73.5	2.9	262	1	S25252	streptomycin 3 - S
1148	73.5	2.9	297	2	T25652	degenerin 1 (DEG-1
1149	73.5	2.9	319	2	A97040	hypothetical prote
1150	73.5	2.9	335	1	KHBOB	cathepsin B (EC 3.
1151	73.5	2.9	366	2	C83034	probable oxidoredu
1152	73.5	2.9	373	2	T22300	hypothetical prote
1153	73.5	2.9	412	2	G82406	long-chain fatty a
1154	73.5	2.9	432	1	S18932	u-plasminogen acti
1155	73.5	2.9	433	2	B29345	steroid hormone re
1156	73.5	2.9	437	2	S14956	alpha-amylase (EC
1157	73.5	2.9	449	2	T14376	self-incompatibili
1158	73.5	2.9	479	2	T23266	hypothetical prote
1159	73.5	2.9	499	2	A56021	probable cell divi
1160	73.5	2.9	564	2	T21983	hypothetical prote
1161	73.5	2.9	565	2	T16408	hypothetical prote
1162	73.5	2.9	617	2	S48160	metalloproteinase
1163	73.5	2.9	797	2	T05247	methionine-tRNA li
1164	73.5	2.9	1159	2	T15963	hypothetical prote
1165	73.5	2.9	1294	2	S01085	hypothetical prote
1166	73.5	2.9	1363	1	VGIHLY	E2 glycoprotein pr
1167	73.5	2.9	1805	2	T21888	hypothetical prote
1168	73.5	2.9	2148	1	A56081	insulin receptor -
1169	73.5	2.9	2150	2	T32497	hypothetical prote
1170	73.5	2.9	3163	2	AB0233	yersiniabactin bio
1171	73.5	2.9	3163	2	T17440	probable polyketid
1172	73.5	2.9	3190	2	T13828	CREB-binding prote
1173	73	2.9	177	2	S37650	high-sulfur kerati
1174	73	2.9	247	2	S33196	osmotin-like prote
1175	73	2.9	247	2	S33197	osmotin-like prote
1176	73	2.9	260	1	A46517	CD27 antigen precu
1177	73	2.9	266	2	I49051	Ly-49F-GE antigen
1178	73	2.9	271	2	T40238	hypothetical prote
1179	73	2.9	281	2	S39495	u-plasminogen acti
1180	73	2.9	302	2	H87476	conserved hypothet
1181	73	2.9	314	2	T28879	hypothetical prote
1182	73	2.9	320	2	B83238	probable oxidoredu
1183	73	2.9	323	2	T24836	hypothetical prote
1184	73	2.9	346	2	S62197	molybdenum formylm
1185	73	2.9	347	2	JQ2359	wheat aluminum ind
1186	73	2.9	392	2	T25213	hypothetical prote
1187	73	2.9	395	1	T45547	arylsulfatase acti
1188	73	2.9	410	2	E85617	hypothetical prote
1189	73	2.9	410	2	G90753	hypothetical prote
1190	73	2.9	435	2	S40993	hypothetical prote
1191	73	2.9	459	2	I48854	gene murine tumour
1192	73	2.9	474	2	B38634	tumor necrosis fac
1193	73	2.9	486	2	S49820	PRL1 protein - Ara
1194	73	2.9	533	2	S18539	actVA-1 protein -
1195	73	2.9	553	2	S38786	gene F protein - N
1196	73	2.9	553	2	S23622	gene F protein - N
1197	73	2.9	554	2	D72760	hypothetical prote
1198	73	2.9	559	1	A35029	t-plasminogen acti
1199	73	2.9	568	2	S42225	major envelope gly
1200	73	2.9	575	1	VCLJHD	env polyprotein pr
1201	73	2.9	616	2	A55796	ecarin precursor -
1202	73	2.9	617	2	T52499	ferredoxin oxidore
1203	73	2.9	681	2	T23455	hypothetical prote
1204	73	2.9	769	2	T45854	hypothetical prote
1205	73	2.9	852	2	A34373	histidine-rich cal
1206	73	2.9	873	1	I48952	VLDL receptor prec
1207	73	2.9	903	2	S60257	meltrin alpha - mo
1208	73	2.9	951	2	T00017	gene ADAMTS-1 prot
1209	73	2.9	961	2	JC2200	alpha-mannosidase
1210	73	2.9	1128	2	AH1949	hypothetical prote
1211	73	2.9	1187	2	T18355	hypothetical prote
1212	73	2.9	1398	2	T18350	probable pol polyp
1213	73	2.9	1797	2	T21889	hypothetical prote
1214	73	2.9	1816	1	S68960	laminin alpha-4 ch
1215	73	2.9	1958	2	T39808	hypothetical prote
1216	73	2.9	2499	1	A30788	mannose 6-phosphat
1217	73	2.9	3229	2	S27852	probable cell-surf
1218	73	2.9	3442	2	E82589	hemagglutinin-like
1219	73	2.9	3455	2	B82519	hemagglutinin-like
1220	72.5	2.9	50	2	A61215	transforming growt
1221	72.5	2.9	139	2	I47207	Ig heavy chain var
1222	72.5	2.9	164	2	T24272	hypothetical prote
1223	72.5	2.9	172	1	KRSHHA	keratin high-sulfu
1224	72.5	2.9	211	2	C82381	pyridoxamine 5'-ph
1225	72.5	2.9	237	2	E90919	interrupted beta-D
1226	72.5	2.9	237	2	B85768	partial beta-D-glu
1227	72.5	2.9	238	2	F84527	hypothetical prote
1228	72.5	2.9	248	1	LNDGPS	pulmonary surfacta
1229	72.5	2.9	248	2	E71602	probable integral
1230	72.5	2.9	266	2	A90436	enoyl CoA hydratas
1231	72.5	2.9	268	2	T19697	hypothetical prote
1232	72.5	2.9	286	2	T35001	probable respirato
1233	72.5	2.9	291	2	C60940	apolipoprotein E -
1234	72.5	2.9	372	2	JC5377	L-selectin precurs
1235	72.5	2.9	384	2	B87427	hypothetical prote
1236	72.5	2.9	394	2	S20450	S-locus-specific g
1237	72.5	2.9	435	2	E96784	hypothetical prote
1238	72.5	2.9	445	2	S42281	S-locus glycoprote
1239	72.5	2.9	445	2	JQ1733	self-incompatibili
1240	72.5	2.9	487	2	C70830	probable PPE prote
1241	72.5	2.9	487	2	JC7126	testis zinc finger
1242	72.5	2.9	513	2	S28358	prespore vesicle p
1243	72.5	2.9	522	2	D96764	unknown protein F2
1244	72.5	2.9	628	2	AF2393	hypothetical prote
1245	72.5	2.9	692	2	T32980	hypothetical prote
1246	72.5	2.9	761	2	T09052	hypothetical prote
1247	72.5	2.9	843	1	A27340	complement C7 prec
1248	72.5	2.9	975	2	I48974	receptor-protein t
1249	72.5	2.9	1070	2	T31069	tolloid-BMP-1 like
1250	72.5	2.9	1197	1	VGVURF	M polyprotein - Ri
1251	72.5	2.9	1363	1	VGIHVA	E2 glycoprotein pr
1252	72.5	2.9	1363	1	VGIHL9	E2 glycoprotein pr
1253	72.5	2.9	1363	2	S44240	surface protein -
1254	72.5	2.9	1416	2	E88550	protein ZC84.1 [im
1255	72.5	2.9	1566	2	T20058	hypothetical prote
1256	72	2.8	92	2	D37057	epithelial cell gl
1257	72	2.8	173	2	H69079	conserved hypothet
1258	72	2.8	214	2	T20056	hypothetical prote
1259	72	2.8	313	2	S44208	extracellular matr
1260	72	2.8	325	2	T09613	probable GTP-bindi
1261	72	2.8	333	1	KHRTH	cathepsin H (EC 3.
1262	72	2.8	348	2	B48435	cysteine proteinas
1263	72	2.8	389	2	H82448	aminotransferase,
1264	72	2.8	429	2	T14417	S-locus-specific g
1265	72	2.8	433	1	UKMS	u-plasminogen acti
1266	72	2.8	437	2	S24546	S-locus glycoprote
1267	72	2.8	499	2	E87416	monooxygenase, fla
1268	72	2.8	523	2	T36968	probable phytoene
1269	72	2.8	584	1	C8HUA	complement C8 alph
1270	72	2.8	631	2	JC2345	kexin-like protein

1271	72	2.8	644	2	JC2346	kexin-like protein
1272	72	2.8	693	2	T25878	hypothetical prote
1273	72	2.8	730	2	I52632	sodium-dependent n
1274	72	2.8	792	2	S72831	hypothetical prote
1275	72	2.8	854	2	T14377	S-receptor kinase
1276	72	2.8	970	2	I78842	receptor protein-t
1277	72	2.8	990	1	G46335	env polyprotein pr
1278	72	2.8	1016	2	G86295	hypothetical prote
1279	72	2.8	1074	2	JC5928	semaphorin F precu
1280	72	2.8	1148	1	GNVUNE	M polyprotein prec
1281	72	2.8	1513	2	T23681	hypothetical prote
1282	72	2.8	1609	2	E87243	probable cation tr
1283	72	2.8	1661	2	T31330	head-activator bin
1284	72	2.8	2796	2	JC4743	fatty-acid synthas
1285	71.5	2.8	82	2	A61040	transforming growt
1286	71.5	2.8	87	2	T00564	gibberellin-regula
1287	71.5	2.8	158	2	T07597	proteinase inhibit
1288	71.5	2.8	159	1	S27195	transforming growt
1289	71.5	2.8	159	1	WFRT1	transforming growt
1290	71.5	2.8	159	2	I57497	transforming growt
1291	71.5	2.8	161	2	T21405	hypothetical prote
1292	71.5	2.8	166	2	T33970	hypothetical prote
1293	71.5	2.8	178	2	T29536	hypothetical prote
1294	71.5	2.8	184	2	AH0357	fimbrial protein [
1295	71.5	2.8	188	2	JC6547	high sulfur protei
1296	71.5	2.8	195	2	T04161	trypsin inhibitor
1297	71.5	2.8	195	2	T19617	hypothetical prote
1298	71.5	2.8	219	2	T27105	hypothetical prote
1299	71.5	2.8	237	2	B55857	klcB protein - pla
1300	71.5	2.8	242	2	T29699	hypothetical prote
1301	71.5	2.8	255	2	I38426	lymphocyte activat
1302	71.5	2.8	300	2	JC5714	G protein-coupled
1303	71.5	2.8	319	2	AE0759	CbiB protein [impo
1304	71.5	2.8	345	2	A05279	surface antigen 51
1305	71.5	2.8	354	2	T22274	hypothetical prote
1306	71.5	2.8	357	2	T23460	hypothetical prote
1307	71.5	2.8	358	2	T17619	hypothetical prote
1308	71.5	2.8	380	2	A42832	factor VIII-associ
1309	71.5	2.8	400	2	JC4591	alpha-1,3 fucosylt
1310	71.5	2.8	414	2	E81201	cell division prot
1311	71.5	2.8	414	2	F81776	cell division prot
1312	71.5	2.8	423	2	H83603	hypothetical prote
1313	71.5	2.8	437	2	JQ1109	S-locus-specific g
1314	71.5	2.8	476	2	T25736	hypothetical prote
1315	71.5	2.8	488	1	EXHU	coagulation factor
1316	71.5	2.8	505	1	P1WL39	L1 protein - human
1317	71.5	2.8	505	2	A53214	dystrophin-associa
1318	71.5	2.8	530	2	T30505	hypothetical prote
1319	71.5	2.8	536	2	T28022	hypothetical prote
1320	71.5	2.8	544	2	S52477	disintegrin (EC 3.
1321	71.5	2.8	570	2	T30527	hypothetical prote
1322	71.5	2.8	641	2	A39961	choline O-acetyltr
1323	71.5	2.8	661	2	I52603	MPS1 protein - mou
1324	71.5	2.8	667	2	T01999	hypothetical prote
1325	71.5	2.8	744	2	A43353	ascites sialoglyco
1326	71.5	2.8	748	2	S66129	disintegrin (EC 3.
1327	71.5	2.8	756	2	G86150	F22M8.3 protein -
1328	71.5	2.8	852	1	VCLJGG	env polyprotein pr
1329	71.5	2.8	902	2	T01127	curly leaf protein
1330	71.5	2.8	955	2	T18435	hypothetical prote
1331	71.5	2.8	1191	2	S76414	beta transducin-li
1332	71.5	2.8	1391	2	T20406	hypothetical prote
1333	71.5	2.8	1653	2	T14758	hypothetical prote
1334	71.5	2.8	2054	2	T32413	probable acetyl-Co
1335	71.5	2.8	2101	2	S57245	insulin receptor (
1336	71.5	2.8	2414	2	A54277	transcription adap
1337	71.5	2.8	3033	1	GNWVJ8	genome polyprotein
1338	71	2.8	205	2	T14745	hypothetical prote
1339	71	2.8	215	2	G85849	probable transcrip
1340	71	2.8	215	2	F91005	probable transcrip
1341	71	2.8	245	2	S12089	hypothetical prote
1342	71	2.8	300	2	G70719	hypothetical prote
1343	71	2.8	313	2	AF1973	hypothetical prote
1344	71	2.8	318	2	E87929	protein T22H2.6 [i
1345	71	2.8	335	2	T32657	hypothetical prote
1346	71	2.8	345	2	T25138	hypothetical prote
1347	71	2.8	348	2	JQ0431	hypothetical 35.5K
1348	71	2.8	358	2	T25137	hypothetical prote
1349	71	2.8	361	2	A75350	phospho-2-dehydro-
1350	71	2.8	363	2	I38937	DNA/RNA-binding pr
1351	71	2.8	372	2	A42778	agglutinin precurs
1352	71	2.8	377	2	JC7535	chitinase (EC 3.2.
1353	71	2.8	384	2	G83040	hypothetical prote
1354	71	2.8	388	2	A88949	protein R09B5.5 [i
1355	71	2.8	394	2	A70504	probable PPE prote
1356	71	2.8	459	2	B58851	NADH2 dehydrogenas
1357	71	2.8	501	2	I39360	IEF SSP 9502 - hum
1358	71	2.8	511	2	S10527	endoglucanase B pr
1359	71	2.8	537	2	B33485	spore coat protein
1360	71	2.8	561	2	T27318	hypothetical prote
1361	71	2.8	580	2	D84772	probable sugar tra
1362	71	2.8	613	2	A88448	protein C45G9.6 [i
1363	71	2.8	721	2	A56352	mitogen-activated
1364	71	2.8	727	2	G02093	glycerol-3-phospha
1365	71	2.8	728	2	I65413	sodium-dependent n
1366	71	2.8	745	2	T07184	subtilisin-like pr
1367	71	2.8	756	2	S47656	tMDC II protein -
1368	71	2.8	802	2	T24293	hypothetical prote
1369	71	2.8	809	2	T32945	hypothetical prote
1370	71	2.8	895	2	T49010	hypothetical prote
1371	71	2.8	934	1	A34372	complement C6 prec
1372	71	2.8	949	2	T24294	hypothetical prote
1373	71	2.8	1037	2	A60163	glycoprotein IIb -
1374	71	2.8	1215	2	E70614	hypothetical prote
1375	71	2.8	1246	2	C36806	hypothetical prote
1376	71	2.8	1323	2	E88257	protein let-23 [im
1377	71	2.8	1356	2	T18521	beta transducin-li
1378	71	2.8	1374	2	S70712	protein-tyrosine k
1379	71	2.8	1551	2	AB2410	WD-repeat protein
1380	71	2.8	3600	2	D86161	F1003.12 protein -
1381	70.5	2.8	145	2	T28944	hypothetical prote
1382	70.5	2.8	146	2	JC7135	agkisacutacin beta
1383	70.5	2.8	149	2	T25246	hypothetical prote
1384	70.5	2.8	182	2	A36686	ultra-high-sulfur
1385	70.5	2.8	264	1	A47737	osteonectin precur
1386	70.5	2.8	294	2	T23916	hypothetical prote
1387	70.5	2.8	296	2	H96781	unknown protein F2
1388	70.5	2.8	314	2	C29960	Balbiani ring 2 ch
1389	70.5	2.8	333	2	AI2485	hypothetical prote
1390	70.5	2.8	335	2	A40036	apoptosis-mediatin
1391	70.5	2.8	341	2	JE0325	LIM protein - huma
1392	70.5	2.8	351	2	G96027	probable 3-carboxy
1393	70.5	2.8	353	2	D96596	hypothetical prote
1394	70.5	2.8	356	2	T20656	hypothetical prote
1395	70.5	2.8	382	2	S12355	xcpY protein - Pse
1396	70.5	2.8	382	2	T27058	hypothetical prote
1397	70.5	2.8	384	2	T29787	hypothetical prote
1398	70.5	2.8	410	2	T23264	hypothetical prote
1399	70.5	2.8	416	2	A37877	hemorrhagic protei
1400	70.5	2.8	455	2	G75473	probable carotenoi
1401	70.5	2.8	457	2	A53669	streptogrisin C (E
1402	70.5	2.8	470	2	F85164	hypothetical prote
1403	70.5	2.8	472	1	A26730	ovoinhibitor precu
1404	70.5	2.8	504	2	T50983	probable pleiotrop
1405	70.5	2.8	514	2	A96671	Ammonium transport
1406	70.5	2.8	517	2	D84512	hypothetical prote
1407	70.5	2.8	535	2	E87656	hypothetical prote
1408	70.5	2.8	615	2	F82132	probable peptidase
1409	70.5	2.8	628	2	JQ0110	hypothetical 69K p
1410	70.5	2.8	660	2	S71949	metalloproteinase
1411	70.5	2.8	690	2	B86296	hypothetical prote
1412	70.5	2.8	697	2	C75525	molybdopterin oxid
1413	70.5	2.8	738	2	D86345	hypothetical prote
1414	70.5	2.8	752	2	T20871	hypothetical prote
1415	70.5	2.8	760	2	D83743	xanthine dehydroge
1416	70.5	2.8	760	2	A40195	meprin A (EC 3.4.2

1417	70.5	2.8	775	2	F98136	hypothetical prote
1418	70.5	2.8	788	1	I59282	diacylglycerol kin
1419	70.5	2.8	795	2	T20609	hypothetical prote
1420	70.5	2.8	800	2	AE3151	glucoamylase [impo
1421	70.5	2.8	837	1	A29512	LDL receptor precu
1422	70.5	2.8	865	2	B96558	probable protein k
1423	70.5	2.8	872	2	T30237	hypothetical prote
1424	70.5	2.8	873	1	QRRBVD	VLDL receptor prec
1425	70.5	2.8	941	1	A55195	chordin precursor
1426	70.5	2.8	955	2	A45441	thrombospondin 4 -
1427	70.5	2.8	996	2	G87687	hypothetical prote
1428	70.5	2.8	1036	2	T17405	scavenger receptor
1429	70.5	2.8	1053	2	S46199	probable complemen
1430	70.5	2.8	1126	2	A96032	probable two-compo
1431	70.5	2.8	1209	2	A49440	chromosome disjunc
1432	70.5	2.8	1260	1	TVRTNU	protein-tyrosine k
1433	70.5	2.8	1363	2	S44241	surface protein -
1434	70.5	2.8	1662	1	H71402	probable kinesin -
1435	70.5	2.8	2311	1	TVCHSR	kinase-related pro
1436	70.5	2.8	2514	2	F81045	hemagglutinin/hemo
1437	70.5	2.8	2703	2	H81193	hemagglutinin/hemo
1438	70	2.8	94	2	C37057	fibronectin recept
1439	70	2.8	115	2	A96909	ferredoxin [import
1440	70	2.8	134	2	E72532	hypothetical prote
1441	70	2.8	191	2	F82725	hypothetical prote
1442	70	2.8	232	2	E97469	hypothetical 23.8K
1443	70	2.8	232	2	AB2688	Hemolysin III [imp
1444	70	2.8	258	2	A71282	conserved hypothet
1445	70	2.8	282	2	E70890	hypothetical prote
1446	70	2.8	327	2	G82748	hypothetical prote
1447	70	2.8	335	2	T31561	hypothetical prote
1448	70	2.8	335	2	T31559	hypothetical prote
1449	70	2.8	335	2	T31560	hypothetical prote
1450	70	2.8	335	2	B82220	hypothetical prote
1451	70	2.8	340	2	S58770	cathepsin B (EC 3.
1452	70	2.8	372	2	H69426	probable transamin
1453	70	2.8	379	2	T40312	probable splicing
1454	70	2.8	391	2	AG3243	conjugal transfer
1455	70	2.8	405	1	JQ2386	3-oxoacyl-[acyl-ca
1456	70	2.8	405	2	T08521	tniQ protein homol
1457	70	2.8	414	1	S05441	cytochrome b5-rela
1458	70	2.8	419	2	T07817	S-locus-specific g
1459	70	2.8	421	2	T03421	traB protein - Agr
1460	70	2.8	425	2	T18592	hypothetical prote
1461	70	2.8	435	2	H72379	ammonium transport
1462	70	2.8	466	1	I46347	exo-alpha-sialidas
1463	70	2.8	474	2	A75276	sensor histidine k
1464	70	2.8	495	2	S32179	tniQ protein homol
1465	70	2.8	500	2	AE1963	hypothetical prote
1466	70	2.8	512	2	T37819	probable zinc meta
1467	70	2.8	525	1	S38794	cellulose 1,4-beta
1468	70	2.8	532	2	JC1392	monophenol monooxy
1469	70	2.8	532	2	JC5412	epidermal growth f
1470	70	2.8	540	2	B47417	insulin receptor-r
1471	70	2.8	588	2	T07085	probable lysine-tR
1472	70	2.8	600	2	T18593	hypothetical prote
1473	70	2.8	602	2	A96254	exsE protein (AJ22
1474	70	2.8	651	2	JC7705	death receptor-6 -
1475	70	2.8	686	2	AI0803	conserved hypothet
1476	70	2.8	721	2	JC4643	lanosterol synthas
1477	70	2.8	754	2	S47268	endothelin-convert
1478	70	2.8	758	2	A54667	endothelin convert
1479	70	2.8	777	2	I48100	ADAM 5 protein pre
1480	70	2.8	780	2	A48143	HF-1 regulatory el
1481	70	2.8	808	2	A41538	ATP-binding casset
1482	70	2.8	809	2	B83409	hypothetical prote
1483	70	2.8	847	2	D72860	viral capsid assoc
1484	70	2.8	859	2	S24571	env protein - huma
1485	70	2.8	942	2	S49109	spherulin - Melolo
1486	70	2.8	951	2	T45726	hypothetical prote
1487	70	2.8	961	2	E86245	hypothetical prote
1488	70	2.8	977	2	S49004	tyrosine kinase Mp
1489	70	2.8	1134	2	C88040	protein F47F6.5 [i
1490	70	2.8	1245	1	VHWVB2	structural polypro
1491	70	2.8	1252	2	S36016	oocyst wall protei
1492	70	2.8	1369	2	S70713	protein-tyrosine k
1493	70	2.8	1782	2	S45289	vitellogenin precu
1494	70	2.8	2470	2	I50726	cation-independent
1495	69.5	2.7	50	2	A48545	transforming growt
1496	69.5	2.7	147	2	A39091	phospholipase A2 i
1497	69.5	2.7	160	1	WFHU1	transforming growt
1498	69.5	2.7	165	2	E64758	membrane protein y
1499	69.5	2.7	172	2	E83264	hypothetical prote
1500	69.5	2.7	189	2	C98167	hypothetical prote

ALIGNMENTS

RESULT 1
S68691
neutrophil granules matrix glycoprotein SGP28 precursor - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68691; S74313; S68683
R;Kjeldsen, L.; Cowland, J.B.; Johnsen, A.H.; Borregaard, N.
FEBS Lett. 380, 246-250, 1996
A;Title: SGP28, a novel matrix glycoprotein in specific granules of human neutrophils wi
A;Reference number: S68691; MUID:96186934; PMID:8601434
A;Accession: S68691
A;Molecule type: mRNA
A;Residues: 1-245 <KJE>
A;Cross-references: UNIPROT:P54108; EMBL:X94323; NID:g1213612; PIDN:CAA63984.1; PID:g121
A;Accession: S74313
A;Molecule type: protein
A;Residues: 33-83;96-143;165-217;221-226 <KJL>
R;Kraetzschmar, J.; Haendler, B.; Eberspaecher, U.; Roosterman, D.; Donner, P.; Schleuni
Eur. J. Biochem. 236, 827-836, 1996
A;Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure and
A;Reference number: S68681; MUID:96270732; PMID:8665901
A;Accession: S68683
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-105,'S',107-245 <KRA>
A;Cross-references: EMBL:X95240; NID:g1262818; PIDN:CAA64527.1; PID:g1262819
C;Genetics:
A;Gene: SGP28
C;Superfamily: cysteine-rich secretory protein 1
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-245/Product: neutrophil granules matrix glycoprotein SGP28 #status predicted <MAT>

Query Match 9.9%; Score 250; DB 2; Length 245;
Best Local Similarity 27.1%; Pred. No. 1.7e-11;
Matches 76; Conservative 44; Mismatches 108; Indels 52; Gaps 12;

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Qy          13 LLAVLLALLGTTWAEVWP--PQLQEQAPMAGALNRKESFL---LLSLHNRLRSWVQPPAA 67
               |  ||| |:    | : |  |  ::: |    ||   :: :   ::: || ||  | |||
Db           3 LFPVLLFLV----AGLLPSFPANEDKDPAFTALLTTQTQVQREIVNKHNELRRAVSPPAR 58

Qy          68 DMRRLDWSDSLAQLAQARAALCGI----PTPSLASGLWRTLQVGWNMQLLPAGLASFVEV 123
               :| :::|:    |  ||  | |       |   : |     |: | |: :  |  :|: :
Db          59 NMLKMEWNKEAAANAQKWANQCNYRHSNPKDRMTS-----LKCGENLYMSSAP-SSWSQA 112

Qy         124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYS 183
               :  || |   :    |    ||   ||||:|| :|  :|||   |   :     :|| |
Db         113 IQSWFDEYNDFDFGVGPKTPNAVVGHYTQVVWYSSYLVGCGNAYCPNQKVLKYYYVCQYC 172

Qy         184 PGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLN 243
               | |||    :  :||::|| |: |  :             |||    | |:
Db         173 PAGNWA--NRLYVPYEQGAPCASCPDNCD---------DGLC---TNGCK---------- 208

Qy         244 ISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREE-ECSCVC 282
                 : :|          :: :| | |   |:  : || |
Db         209 YEDLYSNCK--------SLKLTLTCKHQLVRDSCKASCNC 240
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RESULT 2
S52781
neurocan - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52781
R;Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
submitted to the EMBL Data Library, February 1995
A;Description: Amino acid sequence of mouse neurocan and brevican and their different ex
A;Reference number: S52781
A;Accession: S52781
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1268 <RAU>
A;Cross-references: UNIPROT:P55066; EMBL:X84727; NID:g758629; PIDN:CAA59216.1; PID:g7586
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
F;176-253/Domain: link protein repeat homology <LNK1>
F;274-355/Domain: link protein repeat homology <LNK2>
F;964-995/Domain: EGF homology <EGF>
F;1040-1160/Domain: C-type lectin homology <LCH>
F;1167-1223/Domain: complement factor H repeat homology <FHD>

  Query Match             9.3%;  Score 236;  DB 2;  Length 1268;
  Best Local Similarity   25.3%;  Pred. No. 9.2e-10;
  Matches   73;  Conservative   39;  Mismatches  119;  Indels   58;  Gaps   12;

Qy        177 AFVCAYSPGGNWEVNGKTIIPYKKGAWCSLC-----TASVSGCFKAWDHAGGLCEVPRNP 231
              | | :  | | |::   |:||   |   |:      : || |    |:      | | :|
Db        908 ASVSSGEPTGLWDI-PSTLIPVSLGLDESVLNVVAESPSVEG---FWEEVASGQEDPTDP 963

Qy        232 CRMSCQNHGRLNISTCH-------CHCPPGYTGRYCQV-----RCSLQCVHGRFREEECS 279
                |:|:  |:  |||       | |  || | |::      ||  | :|    :| :
Db        964 ----CENNPCLHGGTCHTNGTVYGCSCDQGYAGENCEIDIDDCLCS-PCENGGTCIDEVN 1018

Qy        280 ---CVCDIGYGGAQCATKVHFPFHTCDL---RIDGDCFMVSSEADTYYRARMKCQRKGGV 333
                |:|   |||:|          ||    :  | |:   :    :  |   |:|: |
Db       1019 GFICLCLPSYGGSLCEKDT----EGCDRGWHKFQGHCYRYFAHRRAWEDAERDCRRRAGH 1074

Qy        334 LAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATGEHQAFT 393
              |  : | :    :               : |   | ||||  :| :  |:|       :
Db       1075 LTSVHSPEEHKFI---------------NSFGHENSWIGLNDRTVERDFQWTDNTGLQYE 1119

Qy        394 SFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRYICQ 442
              ::   ||||          |  :|| : |  :  |||  |     |:|:
Db       1120 NWREKQPDNF-------FAGGEDCVVMVAHESGRWNDVPCNYNLPYVCK 1161


RESULT 3
JC4131
glioma pathogenesis-related protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 04-Mar-2000
C;Accession: JC4131
R;Murphy, E.V.; Zhang, Y.; Zhu, W.; Biggs, J.
Gene 159, 131-135, 1995
A;Title: The human glioma pathogenesis-related protein is structurally related to plant
A;Reference number: JC4131; MUID:95331646; PMID:7607567
A;Accession: JC4131
A;Molecule type: mRNA
A;Residues: 1-219 <MUR>
A;Cross-references: GB:U16307; NID:g1100927; PIDN:AAA82731.1; PID:g847722
A;Experimental source: brain tumor
C;Genetics:
A;Gene: GDB:GLIPR
A;Cross-references: GDB:683195
C;Superfamily: yellowjacket venom allergen antigen 5
C;Keywords: brain

  Query Match             9.2%;  Score 232;  DB 2;  Length 219;
  Best Local Similarity   32.4%;  Pred. No. 3.3e-10;
  Matches   58;  Conservative   28;  Mismatches   61;  Indels   32;  Gaps    7;

Qy         47 ESFL--LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIP----------T 93
              | |:   : :||: || |:| |:||  : |  :|||:|:| |: |
Db         21 EDFIKDCVRIHNKFRSEVKPTASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPHKLH 80

Qy         94 PSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQL 153
              |:  |       :| |:      : |    :: |: | | |:     | :   | ||||:
Db         81 PNFTS-------LGENIWTGSVPIFSVSSAITNWYDEIQDYNFKTRICKK--VCGHYTQV 131

Qy        154 VWATSSQLGCGRHLCS--AGQTAIE---AFVCAYSPGGNWEVNGKTIIPYKKGAWCSLC 207
              ||| | ::||     |   :|  |:     |:| | ||||:        |||:|| || |
Db        132 VWADSYKVGCAVQFCPKVSGFDALSNGAHFICNYGPGGNYPT-----WPYKRGATCSAC 185


RESULT 4
JC5308
testis-specific, vespid, and pathogenesis-related protein 1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 01-May-1997 #sequence_revision 01-May-1997 #text_change 09-Jul-2004
C;Accession: JC5308; PC4311
R;Rich, T.; Chen, P.; Furman, F.; Huynh, N.; Israel, M.A.
Gene 180, 125-130, 1996
A;Title: RTVP-1, a novel human gene with sequence similarity to genes of diverse species
A;Reference number: JC5308; MUID:97128816; PMID:8973356
A;Accession: JC5308
A;Molecule type: mRNA
A;Residues: 1-266 <RIC1>
A;Cross-references: UNIPROT:P48060; EMBL:X91911; NID:g1030052; PIDN:CAA63005.1; PID:g103
A;Accession: PC4311
A;Molecule type: protein
A;Residues: 97-100;114-120;134-144 <RIC2>
A;Experimental source: brain tumor cell
C;Genetics:
A;Gene: rtvp-1
C;Superfamily: yellowjacket venom allergen antigen 5
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-266/Product: testis-specific, vespid, and pathogenesis-related protein 1 #status pr
F;233-255/Domain: transmembrane #status predicted <TMM>

  Query Match             9.1%;  Score 231;  DB 2;  Length 266;
  Best Local Similarity   32.4%;  Pred. No. 4.8e-10;
  Matches   58;  Conservative   27;  Mismatches   62;  Indels   32;  Gaps    7;

Qy         47 ESFL--LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIP----------T 93
              | |:   .: :||: || |:| |:||  : |  :|||:|:| |: |
Db         31 EDFIKDCVRIHNKFRSEVKPTASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPHKLH 90

Qy         94 PSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQL 153
              |:  |       :| |:      : |    :: |: | | |:     | :   | ||||:
Db         91 PNFTS-------LGENIWTGSVPIFSVSSAITNWYDEIQDYDFKTRICKK--VCGHYTQV 141

Qy        154 VWATSSQLGCGRHLCS--AGQTAIE---AFVCAYSPGGNWEVNGKTIIPYKKGAWCSLC 207
              ||| | ::||     |   :|  |:     |:| | ||||:        |||:|| || |
Db        142 VWADSYKVGCAVQFCPKVSGFDALSNGAHFICNYGPGGNYPT-----WPYKRGATCSAC 195


RESULT 5
T16415
hypothetical protein F48E8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16415
R;Kirsten, J.
submitted to the EMBL Data Library, March 1995
A;Description: The sequence of C. elegans cosmid F48E8.
A;Reference number: S59413
A;Accession: T16415
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-312 <KIR>
A;Cross-references: UNIPROT:Q09566; EMBL:U23514; NID:g746484; PID:g746485; PIDN:AAC46538
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F48E8.1
A;Introns: 28/1; 94/3; 153/3; 174/3; 226/3
```

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  Query Match             8.9%;  Score 224;  DB 2;  Length 312;
  Best Local Similarity   29.7%;  Pred. No. 1.9e-09;
  Matches   69;  Conservative   28;  Mismatches   75;  Indels   60;  Gaps   13;

Qy         29 WPPQLQEQAPMAGALNRKE---SFL---LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLA 82
              :|   |      :| |:| |    :|    :   ||| |  |  ||:||  | ||| ||  |
Db         59 FPSHFQSD---SGLLSRSEHPNEYLKKWITHEHNRYRRMV--PASDMNMLYWSDELAASA 113

Qy         83 QARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQR----YSHAA 138
              |  |  |           : || |:    |   ::: : :|:|| |        :||
Db        114 QRHADTCDFRHSR------GRINVGENIWAAP--YSNYSDAISIWFNEVHNPRCGCNHAY 165

Qy        139 GECARNATCTHYTQLVWATSSQLGCGRHLCSA-----GQTAIEAFVCAYSPGGNWEVNGK 193
                |     | || |:||| :: :|||   |        |:     ||| |:| ||
Db        166 KHC-----CGHYVQVVWAKTNLVGCGFSRCRDVQGVWGRGHRNVFVCHYNPQGN------ 214

Qy        194 TIIPYKKG--------AW-------CSLCTASVSGCFKAWDHAGGLCEVPRN 230
              |:    :|        |       || | |:   |::      ||| :|:|
Db        215 TVFVTARGQLYAMPAFTWASGDNGKCSNCPANAPACYQ------GLCYMPKN 260


RESULT 6
B33329
cysteine-rich secretory protein 2 type I precursor - human
N;Alternate names: testis-specific protein
C;Species: Homo sapiens (man)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C;Accession: B33329; S68682
R;Kasahara, M.; Gutknecht, J.; Brew, K.; Spurr, N.; Goodfellow, P.N.
Genomics 5, 527-534, 1989
A;Title: Cloning and mapping of a testis-specific gene with sequence similarity to a spe
A;Reference number: A33329; MUID:90129048; PMID:2613236
A;Accession: B33329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-243 <KAS>
A;Cross-references: UNIPROT:P16562; GB:M25532; NID:g339882; PIDN:AAA61220.1; PID:g339883
R;Kraetzschmar, J.; Haendler, B.; Eberspaecher, U.; Roosterman, D.; Donner, P.; Schleuni
Eur. J. Biochem. 236, 827-836, 1996
A;Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure and
A;Reference number: S68681; MUID:96270732; PMID:8665901
A;Accession: S68682
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-243 <KRA>
A;Cross-references: EMBL:X95239; NID:g1262816; PIDN:CAA64526.1; PID:g1262817
C;Genetics:
A;Gene: GDB:TPX1
A;Cross-references: GDB:120760; OMIM:187430
A;Map position: 6p21-6qter
C;Superfamily: cysteine-rich secretory protein 1
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-243/Product: cysteine-rich secretory protein 2 type I #status predicted <MAT>

  Query Match             8.7%;  Score 221;  DB 2;  Length 243;
  Best Local Similarity   28.1%;  Pred. No. 2.4e-09;
  Matches   72;  Conservative   36;  Mismatches   88;  Indels   60;  Gaps   10;

Qy         13 LLAVLL-------------ALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLR 59
              |: |||               ||| |         ||| |              ::: || ||
Db          9 LVTVLLPSLPAEGKDPAFTALLTT--------QLQVQRE------------IVNKHNELR 48

Qy         60 SWVQPPAADMRRLDWSDSLAQLAQARAALCGI----PTPSLASGLWRTLQVGWNMQLLPA 115
                | |||::| :::||  :   ||  | | :    |      |      : | |:  : :
Db         49 KAVSPPASNMLKMEWSREVTTNAQRWANKCTLQHSDPEDRKTS-----TRCGENL-YMSS 102

Qy        116 GLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAI 175
                |:   :  |: |   : :  |  : ||   ||||||| :: |:|||   |    :
Db        103 DPTSWSSAIQSWYDEILDFVYGVGPKSPNAVVGHYTQLVWYSTYQVGCGIAYCPNQDSLK 162

Qy        176 EAFVCAYSPGGNWEVNGKTIIPYKKGAWCS---------LCTAS------VSGCFKAWDH 220
                :|| | | ||  :| |   ||::|  |:         ||| |      :| |    :
Db        163 YYYVCQYCPAGN-NMNRKN-TPYQQGTPCAGCPDDCDKGLCTNSCQYQDLLSNCDSLKNT 220

Qy        221 AGGLCEVPRNPCRMSC 236
                ||   |: :  |: :|
Db        221 AGCEHELLKEKCKATC 236


RESULT 7
S68684
cysteine-rich secretory protein 1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68684
R;Kraetzschmar, J.; Haendler, B.; Eberspaecher, U.; Roosterman, D.; Donner, P.; Schleuni
Eur. J. Biochem. 236, 827-836, 1996
A;Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure and
A;Reference number: S68681; MUID:96270732; PMID:8665901
A;Accession: S68684
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-249 <KRA>
A;Cross-references: UNIPROT:P54107; EMBL:X95237; NID:g1262814; PIDN:CAA64524.1; PID:g126
C;Superfamily: cysteine-rich secretory protein 1
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-249/Product: cysteine-rich secretory protein 1 #status predicted <MAT>

  Query Match             8.4%;  Score 213.5;  DB 2;  Length 249;
  Best Local Similarity   27.2%;  Pred. No. 9.1e-09;
  Matches   66;  Conservative   40;  Mismatches   90;  Indels   47;  Gaps   11;

Qy         31 PQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCG 90
              | :||:               ::::|| ||  | |||::| :: ||:  || |:  :  |
Db         38 PNVQEE-------------IVNIHNALRRRVVPPASNMLKMSWSEEAAQNARIFSKYCD 83

Qy         91 IPTPSLASGLWRTLQ---VGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECAR---N 144
              :   : :: | | |     | || :    : |:  |: :|::|   : |  ||      :
Db         84 M---TESNPLERRLPNTFCGENMHMTSYPV-SWSSVIGVWYSESTSFKH--GEWTTTDDD 137

Qy        145 ATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGGN-WEVNGKTIIPYKKGAW 203
              |  ||||:|||||  :||    |    :    :|| |   ||  |   :   |||  |
Db        138 ITTDHYTQIVWATSYLIGCAIASCRQQGSPRYLYVCHYCHEGNDPETKNE---PYKTGVP 194

Qy        204 CSLCTASVSGCFKAWDHAGGLCE--VPRNPCRMSCQNHGRLNISTCHCHCPPGYTGRYCQ 261
              |  | ::              ||  :  ||| :    :   :|  |   |    | :|:
Db        195 CEACPSN-------------CEDKLCTNPC-IYYDEYFDCDIQVHYLGCNHSTTILFCK 239

Qy        262 VRC 264
                |
Db        240 ATC 242


RESULT 8
S28764
neurocan precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S28764
R;Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, R.U.; Margolis, R.K.
J. Biol. Chem. 267, 19536-19547, 1992
A;Title: Cloning and primary structure of neurocan, a developmentally regulated, aggrega
A;Reference number: S28764; MUID:92406907; PMID:1326557
A;Accession: S28764
A;Molecule type: mRNA
A;Residues: 1-1257 <RAU>
A;Cross-references: UNIPROT:P55067; EMBL:M97161; NID:g205649; PIDN:AAC37679.1; PID:g2056
C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
C;Keywords: chondroitin sulfate proteoglycan; glycoprotein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-1257/Product: neurocan #status predicted <MAT>
F;176-253/Domain: link protein repeat homology <LNK1>
F;274-355/Domain: link protein repeat homology <LNK2>
F;364-366/Region: cell attachment (R-G-D) motif
F;953-984/Domain: EGF homology <EGF>
```

```
F;1029-1149/Domain: C-type lectin homology <LCH>
F;1156-1212/Domain: complement factor H repeat homology <FHD>
F;121,339,737,967,1164/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;372,410/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
F;944/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental

  Query Match             8.4%;  Score 212;  DB 2;  Length 1257;
  Best Local Similarity   24.8%;  Pred. No. 5.7e-08;
  Matches   70;  Conservative   34;  Mismatches  134;  Indels   44;  Gaps   10;

Qy        177 AFVCAYSPGGNWEVNGKTIIPYKKGAWCS--LCTASVSGCFKAWDHAGGLCEVPRNPCRM 234
              | | :  |   |::   |:||   |    |     |   |    |:      | | :||
Db        897 ASVSSGEPTRLWDI-PSTLIPVSLGLDESDLKVVAESPGLEGFWEEVASGQEDPTDPCEN 955

Qy        235 SCQNHG---RLNISTCHCHCPPGYTGRYCQV-----RCSLQCVHGRFREEECS---CVCD 283
              :   ||   | | :   | |  || |  |::      ||  | :|   :| :   |:|
Db        956 NPCLHGGTCRTNGTMYGCSCDQGYAGENCEIDIDDCLCS-PCENGGTCIDEVNGFICLCL 1014

Qy        284 IGYGGAQCATKVHFPFHTCDL---RIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQ 340
              |||  |           ||    :  | |:   :    :  |   |:|: | |  : |
Db       1015 PSYGGNLCEKDT----EGCDRGWHKFQGHCYRYFAHRRAWEDAERDCRRRAGHLTSVHSP 1070

Qy        341 KVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQP 400
              :   :               : |   | ||||  :| :  |:|       : ::   ||
Db       1071 EEHKFI--------------NSFGHENSWIGLNDRTVERDFQWTDNTGLQYENWREKQP 1115

Qy        401 DNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRYICQ 442
              ||          | :|| : |     |||  |    |:|:
Db       1116 DNF-------FAGGEDCVVMVAHENGRWNDVPCNYNLPYVCK 1150


RESULT 9
A49202
cysteine-rich secretory protein-1 - mouse
N;Alternate names: CRISP-1
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A49202
R;Haendler, B.; Kratzschmar, J.; Theuring, F.; Schleuning, W.D.
Endocrinology 133, 192-198, 1993
A;Title: Transcripts for cysteine-rich secretory protein-1 (CRISP-1; DE/AEG) and the nov
A;Reference number: A49202; MUID:93307144; PMID:8319566
A;Accession: A49202
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-244 <HAE>
A;Cross-references: UNIPROT:Q03401; GB:L05559; NID:g309190; PIDN:AAA37460.1; PID:g309191
A;Experimental source: NMRI, epididymis, salivary gland
A;Note: sequence extracted from NCBI backbone (NCBIN:134675, NCBIP:134676)
C;Superfamily: cysteine-rich secretory protein 1

  Query Match             8.3%;  Score 209;  DB 2;  Length 244;
  Best Local Similarity   25.7%;  Pred. No. 1.9e-08;
  Matches   76;  Conservative   44;  Mismatches  110;  Indels   66;  Gaps   15;

Qy         13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFL------LLSLHNRLRSWVQPPA 66
              |: ||  |     | | || | : :     | :  :        ::| ||:||  | |
Db          3 LMLVLFFL-----AAVLPPSLLQDSSQENRLEKLSTTKMSVQEEIVSKHNQLRRMVSPSG 57

Qy         67 ADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRT--LQVGWNMQLLPAGLASFVEVV 124
              :|: :::|:      ||  |  |   | | :    ||   |: | |:  : : |||:   :
Db         58 SDLLKMEWNYDAQVNAQQWADKC---TFSHSPIELRTTNLRCGENL-FMSSYLASWSSAI 113

Qy        125 SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSP 184
               |: | :  ::  |    ::   ||||:|| :: |: ||   |         :|| | |
Db        114 QGWYNEYKDLTYDVGPKQPDSVVGHYTQVVWNSTFQVACGVAECPKNPLRY-YYVCHYCP 172

Qy        185 GGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHA-GGLCEVPRNPCRMSCQNHGRLN 243
              ||::  |:   ||  |  |: |           ||   |||    | |
Db        173 VGNYQ--GRLYTPYTAGEPCASCP----------DHCEDGLC---TNSC---------- 206

Qy        244 ISTCHCHCPPGYTGRY--CQ-VRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVH 296
                        |:  :|  |: ::  | | |    :: |   |        |  |:|
Db        207 ----------GHEDKYTNCKYLKKMLSCEH-ELLKKGCKATC-------LCEGKIH 244


RESULT 10
JE0204
testicular protein Tpx-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE0204
R;Maeda, T.; Sakashita, M.; Ohba, Y.; Nakanishi, Y.
Biochem. Biophys. Res. Commun. 248, 140-146, 1998
A;Title: Molecular cloning of the rat tpx-1 responsible for the interaction between sper
A;Reference number: JE0204; MUID:98340864; PMID:9675100
A;Accession: JE0204
A;Molecule type: mRNA
A;Residues: 1-243 <MAE>
A;Cross-references: UNIPROT:O88205; DDBJ:AB009662; NID:g3374579; PIDN:BAA32029.1; PID:g3
C;Comment: This protein functions as a cell adhesion protein for the association between
C;Genetics:
A;Map position: 17
C;Superfamily: cysteine-rich secretory protein 1

  Query Match             8.2%;  Score 208;  DB 2;  Length 243;
  Best Local Similarity   25.5%;  Pred. No. 2.3e-08;
  Matches   74;  Conservative   41;  Mismatches  113;  Indels   62;  Gaps   13;

Qy         13 LLAVLLALLGT-----TWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAA 67
              : |||| |  |      :| :   |:| |              ::: || ||  | || :
Db         10 VFAVLLPLPPTEGKDPDFATLTTNQIQVQRE------------IIAKHNELRRQVSPPGS 57

Qy         68 DMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLW 127
              :: :::|:    |  ||  |  | |    |         :: | |:  :     |:  |:  |
Db         58 NILKMEWNVQAAANAQKWANNC-ILEHSSTEDRKINIKCGENL-YMSTDPTSWRTVIQSW 115

Qy        128 FAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGGN 187
              : | : :    |     |:   ||||||| :| ::|||    |     |     :|| | | ||
Db        116 YEENENFVFGVG-AKPNSAVGHYTQLVWYSSFKVGCGVAYCPNQDTLKYFYVCHYCPMGN 174

Qy        188 WEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTC 247
                :   |  || :|  |: |    : |          |||     | |              :| |
Db        175 NVMKKST--PYHQGTPCASCP---NNC------DNGLC---TNSCDFEDL------LSNC 214

Qy        248 HCHCPPGYTGRYCQVRCSLQCVHGRFREE-ECSCVCDIGYGGAQCATKVH 296
                          :: |  | |   : : | :|:|:          |:|
Db        215 E------------SLKSSAGCKHELLKAKCEATCLCE---------DKIH 243


RESULT 11
A55535
versican precursor - mouse
N;Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
versican
N;Contains: glial hyaluronate-binding protein
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A55535
R;Ito, K.; Shinomura, T.; Zako, M.; Ujita, M.; Kimata, K.
J. Biol. Chem. 270, 958-965, 1995
A;Title: Multiple forms of mouse PG-M, a large chondroitin sulfate proteoglycan generate
A;Reference number: A55535; MUID:95122551; PMID:7822336
A;Accession: A55535
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2397 <RES>
A;Cross-references: GB:D16263; NID:g862460; PIDN:BAA03796.1; PID:g862461
C;Superfamily: versican; C-type lectin homology; complement factor H repeat homology; EG
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-1654/Domain: versican #status predicted <MAT>
F;167-244/Domain: link protein repeat homology <LNK1>
F;265-346/Domain: link protein repeat homology <LNK2>
F;2095-2126/Domain: EGF homology <EG1>
F;2133-2164/Domain: EGF homology <EG2>
F;2171-2291/Domain: C-type lectin homology <LCH>
```

```
F;2298-2354/Domain: complement factor H repeat homology <FHD>

  Query Match             7.9%;  Score 200;  DB 1;  Length 2397;
  Best Local Similarity   27.0%;  Pred. No. 8.4e-07;
  Matches   65;  Conservative   28;  Mismatches   84;  Indels   64;  Gaps   13;

Qy        224 LCEVPRNPCRMSCQNHGRLNISTCH-------CHCPPGYTGRYCQV----------RCSL 266
              ||:   |||          ||  ||:       | | |||:|  |::          |
Db       2094 LCKT--NPC---------LNGGTCYPTETSYVCTCAPGYSGDQCELDFDECHSNPCRNGA 2142

Qy        267 QCVHG--RFREEECSCVCDIGYGGAQCATKVHPPFHTCDL---RIDGDCFMVSSEADTYY 321
              || |   ||     |:|   | || |         |||    :  | |:   :   |:
Db       2143 TCVDGFNTFR-----CLCLPSYVGALCEQDT----ETCDYGWHKFQGQCYKYFAHRRTWD 2193

Qy        322 RARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDS 381
              |  :|: :|  |  | | : |     :: |:         |::    ||||  |  :
Db       2194 AAERECRLQGAHLTSILSHEEQ----MFVNRV-------GHDYQ----WIGLNDKMFEHD 2238

Qy        382 FRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRYIC 441
              |||  |    : ::   |||:    : ||    :|| :       |||  |     | |
Db       2239 FRWTDGSALQYENWRPNQPDS----FFSAG---EDCVVIIWHENGQWNDVPCNYHLTYTC 2291

Qy        442 Q 442
              :
Db       2292 K 2292


RESULT 12
A60979
versican precursor - human
N;Alternate names: chondroitin sulfate proteoglycan 2; chondroitin sulfate proteoglycan
N;Contains: glial hyaluronate-binding protein
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S06014; S43921; A60979; A30358; A29348; A45131; I54179
R;Zimmermann, D.R.; Ruoslahti, E.
EMBO J. 8, 2975-2981, 1989
A;Title: Multiple domains of the large fibroblast proteoglycan, versican.
A;Reference number: S06014; MUID:90059882; PMID:2583089
A;Accession: S06014
A;Molecule type: mRNA
A;Residues: 1-2409 <ZIM>
A;Cross-references: UNIPROT:P13611; UNIPROT:Q9UCL9; GB:X15998; NID:g37662; PIDN:CAA34128
R;Yao, L.Y.; Moody, C.; Schoenherr, E.; Wight, T.N.; Sandell, L.J.
Matrix Biol. 14, 213-225, 1994
A;Title: Identification of the proteoglycan versican in aorta and smooth muscle cells by
A;Reference number: S43921; MUID:95005762; PMID:7921538
A;Accession: S43921
A;Molecule type: mRNA
A;Residues: 208-440;1094-1385;1910-2246 <YAO>
R;Bignami, A.; Lane, W.S.; Andrews, D.; Dahl, D.
Brain Res. Bull. 22, 67-70, 1989
A;Title: Structural similarity of hyaluronate binding proteins in brain and cartilage.
A;Reference number: A60979; MUID:89229983; PMID:2469524
A;Accession: A60979
A;Molecule type: protein
A;Residues: 171-210;289-303 <BIG>
R;Perides, G.; Lane, W.S.; Andrews, D.; Dahl, D.; Bignami, A.
J. Biol. Chem. 264, 5981-5987, 1989
A;Title: Isolation and partial characterization of a glial hyaluronate-binding protein.
A;Reference number: A30358; MUID:89174663; PMID:2466833
A;Accession: A30358
A;Molecule type: protein
A;Residues: 24-50;80-87,'D',89-119;128-155;167-218;229-259,'IR';261-268;277-283,'G',285-
R;Krusius, T.; Gehlsen, K.R.; Ruoslahti, E.
J. Biol. Chem. 262, 13120-13125, 1987
A;Title: A fibroblast chondroitin sulfate proteoglycan core protein contains lectin-like
A;Reference number: A29348; MUID:88007514; PMID:2820964
A;Accession: A29348
A;Molecule type: mRNA
A;Residues: 1725,'V',1727-2409 <KRU>
A;Cross-references: GB:J02814
R;Perides, G.; Rahemtulla, F.; Lane, W.S.; Asher, R.A.; Bignami, A.
J. Biol. Chem. 267, 23883-23887, 1992
A;Title: Isolation of a large aggregating proteoglycan from human brain.
A;Reference number: A45131; MUID:93054750; PMID:1429726
A;Contents: brain
A;Accession: A45131
A;Molecule type: protein
A;Residues: 21-22,'X',24-37 <PE2>
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:118884)
R;Iozzo, R.V.; Naso, M.F.; Cannizzaro, L.A.; Wasmuth, J.J.; McPherson, J.D.
Genomics 14, 845-851, 1992
A;Title: Mapping of the versican proteoglycan gene (CSPG2) to the long arm of human chr
A;Reference number: I54179; MUID:93122792; PMID:1478664
A;Accession: I54179
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 251-347 <RES>
A;Cross-references: GB:S52488; NID:g263313; PIDN:AAB24878.1; PID:g263314
C;Genetics:
A;Gene: GDB:CSPG2
A;Cross-references: GDB:127873; OMIM:118661
A;Map position: 5q12-5q14
C;Superfamily: versican; C-type lectin homology; complement factor H repeat homology; E
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-2409/Product: proteoglycan 24K core protein #status predicted <MAT>
F;167-244/Domain: link protein repeat homology <LNK1>
F;265-346/Domain: link protein repeat homology <LNK2>
F;559-1654/Domain: chondroitin sulfate attachment #status predicted <GAG>
F;2106-2137/Domain: EGF homology <EG1>
F;2144-2175/Domain: EGF homology <EG2>
F;2182-2302/Domain: C-type lectin homology <LCH>
F;2309-2365/Domain: complement factor H repeat homology <FHD>

  Query Match             7.8%;  Score 196;  DB 1;  Length 2409;
  Best Local Similarity   26.8%;  Pred. No. 1.7e-06;
  Matches   63;  Conservative   27;  Mismatches   83;  Indels   62;  Gaps   12;

Qy        230 NPCRMSCQNHGRLNISTCH-------CHCPPGYTGRYCQV----------RCSLQCVHG- 271
              |||          ||  ||:       | | |||:|  |::          |    || |
Db       2109 NPC---------LNGGTCYPTETSYVCTCVPGYSGDQCELDFDECHSNPCRNGATCVDGF 2159

Qy        272 -RFREEECSCVCDIGYGGAQCATKVHPPFHTCDL---RIDGDCFMVSSEADTYYRARMKC 327
               ||      |:|   | || |         |||    :  | |:   :   |:  | :|
Db       2160 NTFR-----CLCLPSYVGALCEQDT----ETCDYGWHKFQGQCYKYFAHRRTWDAAEREC 2210

Qy        328 QRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATG 387
              : :|  |  | | : |     :: |:         |::    ||||  |  :  |||  |
Db       2211 RLQGAHLTSILSHEEQ----MFVNRV-------GHDYQ----WIGLNDKMFEHDFRWTDG 2255

Qy        388 EHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRYICQ 442
                : ::   |||:    : ||     :|| :       |||  |     | |:
Db       2256 STLQYENWRPNQPDS----FFSAG---EDCVVIIWHENGQWNDVPCNYHLTYTCK 2303


RESULT 13
A33329
testis-specific protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C;Accession: A33329
R;Kasahara, M.; Gutknecht, J.; Brew, K.; Spurr, N.; Goodfellow, P.N.
Genomics 5, 527-534, 1989
A;Title: Cloning and mapping of a testis-specific gene with sequence similarity to a spe
A;Reference number: A33329; MUID:90129048; PMID:2613236
A;Accession: A33329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-243 <KAS>
A;Cross-references: UNIPROT:P16563; GB:M25533; NID:g202126; PIDN:AAA40472.1; PID:g202127
C;Superfamily: cysteine-rich secretory protein 1

  Query Match             7.7%;  Score 193.5;  DB 2;  Length 243;
  Best Local Similarity   24.0%;  Pred. No. 2.8e-07;
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  Matches   63;  Conservative   30;  Mismatches   93;  Indels   77;  Gaps   11;

Qy         51 LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPS-------LASG---- 99
              ::: || ||  | |  :|: :::||       ||  |  | :    |       :   |
Db         41 IVNKHNELRRSVNPTGSDILKMEWSIQATTNAQKWANKCILEHSSKDDRKINIRCGENLY 100

Qy        100 ------LWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQL 153
                  || |                    |:  |: | : : :  |    |:   |||||
Db        101 MSTDPTLWST------------------VIQSWYNENEDFVYGVG-AKPNSAVGHYTQL 140

Qy        154 VWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSG 213
              || :| ::|||   |          :|| | | ||  :   |  ||::|  |: |  :
Db        141 VWYSSFKIGCGIAYCPNQDNLKYFYVCHYCPMGNNVMKKST--PYQQGTPCASCPNN--- 195

Qy        214 CFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRF 273
                       ||     |  ||     |  | |                :: |  | |
Db        196 ----------CE--NGLCTNSCDFEDLL--SNCE------------SLKTSAGCKH-EL 227

Qy        274 REEECSCVCDIGYGGAQCATKVH 296
              : :|   |         |  |:|
Db        228 LKTKCQATC-------LCEDKIH 243


RESULT 14
A47171
chondroitin sulfate proteoglycan PG-M core protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47171
R;Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A;Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during

A;Reference number: A47171; MUID:93300846; PMID:8314802
A;Accession: A47171
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-3562 <SHI>
A;Cross-references: UNIPROT:Q90953; GB:D13542; NID:g391643; PIDN:BAA02742.1; PID:g391644
A;Experimental source: stage 22-23 developing limb buds
A;Note: sequence extracted from NCBI backbone (NCBIN:134456, NCBIP:134457)
C;Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lectin
F;166-243/Domain: link protein repeat homology <LNK1>
F;264-345/Domain: link protein repeat homology <LNK2>
F;3258-3289/Domain: EGF homology <EGF1>
F;3296-3327/Domain: EGF homology <EGF>
F;3334-3454/Domain: C-type lectin homology <LCH>
F;3461-3517/Domain: complement factor H repeat homology <FHD>

  Query Match             7.6%;  Score 191;  DB 2;  Length 3562;
  Best Local Similarity   25.1%;  Pred. No. 5.8e-06;
  Matches   61;  Conservative   35;  Mismatches   91;  Indels   56;  Gaps   13;

Qy        222 GGLCEVP-RNPCRMS-CQNHGRLNISTCH-------CHCPPGYTGRYCQV---------- 262
              |   ::| ::||: : | | |     ||:       | | ||: |  |::
Db       3247 GTAVQIPGQDPCKSNPCLNGG-----TCYPRGSFYICTCLPGFNGEQCELDIDECQSNPC 3301

Qy        263 RCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDL---RIDGDCFMVSSEADT 319
              |    |: |       :|:|   | ||| |         |||    :  | |:   :   |
Db       3302 RNGATCIDGL---NTFTCLCLPSYIGALCEQDT----ETCDYGWHKFQGQCYKYFAHRRT 3354

Qy        320 YYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAK 379
              :  |  :|: :|  |  | | : |     :: |:         |::    |||| |  :
Db       3355 WDTAERECRLQGAHLTSILSHEEQ----VFVNRI-------GHDYQ----WIGLNDKMFE 3399

Qy        380 DSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRY 439
              |||  |   : ::   |||:    : ||    :|| :       |||  |      |
Db       3400 RDFRWTDGSPLQYENWRPNQPDS----FFSAG---EDCVVIIWHENGQWNDVPCNYHLTY 3452

Qy        440 ICQ 442
              |:
Db       3453 TCK 3455


RESULT 15
T14274
versican precursor, splice form V2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14274
R;Schmalfeldt, M.; Dours-Zimmermann, M.T.; Winterhalter, K.H.; Zimmermann, D.R.
J. Biol. Chem. 273, 15758-15764, 1998
A;Title: Versican V2 is a major extracellular matrix component of the mature bovine brai
A;Reference number: Z17954; MUID:98288320; PMID:9624174
A;Accession: T14274
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1643 <SCH>
A;Cross-references: UNIPROT:P81282; EMBL:AF060458; NID:g3253303; PID:g3253304; PIDN:AAC2
A;Experimental source: brain
C;Keywords: glycoprotein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-1643/Product: versican, splice form V2 #status predicted <MAT>
F;57,331,352,817,965,1017,1333,1616,1626/Binding site: carbohydrate (Asn) (covalent) #st

  Query Match             7.5%;  Score 190;  DB 2;  Length 1643;
  Best Local Similarity   26.0%;  Pred. No. 3.2e-06;
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Qy        230 NPCRMSCQNHGRLNISTCH-------CHCPPGYTGRYCQV----------RCSLQCVHG- 271
              |||          ||  ||:       | | |||:|  |::          |    |: |
Db       1343 NPC---------LNGGTCYPTETSYVCTCVPGYSGDRCELDFDECHSNPCRNGATCIDGF 1393

Qy        272 -RFREEECSCVCDIGYGGAQCATKVHFPFHTCDL---RIDGDCFMVSSEADTYYRARMKC 327
               ||     |:|   | || |         |||    :  | |:   :   |:  |  :|
Db       1394 NTFR-----CLCLPSYVGALCEQDT----ETCDYGWHKFQGQCYKYFAHRRTWDAAEREC 1444

Qy        328 QRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATG 387
              : :|  |  | | : |     :: |:         |::    ||||  |  :  |||  |
Db       1445 RLQGAHLTSILSHEEQ----MFVNRV-------GHDYQ----WIGLNDKMFEHDFRWTDG 1489

Qy        388 EHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCKTRNRYICQ 442
                : ::   |||:    : |      :|| :       |||  |     | |:
Db       1490 STLQYENWRPNQPDS----FFSTG---EDCVVIIWHENGQWNDVPCNYHLTYTCK 1537


Search completed: February 11, 2005, 19:05:00
Job time : 65 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 11, 2005, 19:05:46 ; Search time 132 Seconds
(without alignments)
1126.294 Million cell updates/sec

Perfect score: 2529
Sequence: 1 MLHPETSPGRGHLLAVLLAL.....RNRYICQFAQEHISRWGPGS 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
3	2529	100.0	455	9	US-09-944-457-50	Sequence 50, Appl
23	2529	100.0	455	15	US-10-429-667-50	Sequence 50, Appl
24	2529	100.0	455	15	US-10-677-471-50	Sequence 50, Appl
25	2529	100.0	455	15	US-10-677-669-50	Sequence 50, Appl
26	2529	100.0	455	16	US-10-901-400-50	Sequence 50, Appl
27	2529	100.0	455	17	US-10-858-981-50	Sequence 50, Appl
28	2447.5	96.8	446	9	US-09-726-643-47	Sequence 47, Appl
29	2447.5	96.8	446	9	US-09-790-264-2	Sequence 2, Appli
30	2447.5	96.8	446	13	US-10-042-141-47	Sequence 47, Appl
31	2447.5	96.8	446	14	US-10-269-353-2	Sequence 2, Appli
32	2447.5	96.8	446	15	US-10-169-395-5	Sequence 5, Appli
33	2447.5	96.8	446	17	US-10-919-272-47	Sequence 47, Appl
34	2447.5	96.8	446	17	US-10-900-926-2	Sequence 2, Appli
35	2315.5	91.6	420	9	US-09-790-264-4	Sequence 4, Appli
36	2315.5	91.6	420	14	US-10-269-353-4	Sequence 4, Appli
37	2315.5	91.6	420	17	US-10-900-926-4	Sequence 4, Appli
38	2241	88.6	415	15	US-10-309-290-84	Sequence 84, Appl
39	280	11.1	463	14	US-10-387-495-4	Sequence 4, Appli
40	280	11.1	463	15	US-10-429-668-9	Sequence 9, Appli
41	280	11.1	550	15	US-10-429-668-8	Sequence 8, Appli
42	280	11.1	625	15	US-10-429-668-7	Sequence 7, Appli
43	273	10.8	506	15	US-10-429-668-2	Sequence 2, Appli
44	273	10.8	593	15	US-10-429-668-3	Sequence 3, Appli
47	272	10.8	463	9	US-09-905-291A-285	Sequence 285, App
397	272	10.8	463	14	US-10-299-976-285	Sequence 285, App
412	272	10.8	463	14	US-10-299-937-285	Sequence 285, App
538	272	10.8	463	15	US-10-298-993-285	Sequence 285, App
540	272	10.8	463	15	US-10-448-923-285	Sequence 285, App
541	272	10.8	463	15	US-10-449-656-285	Sequence 285, App
542	272	10.8	463	15	US-10-448-713-285	Sequence 285, App
545	272	10.8	463	15	US-10-425-447-285	Sequence 285, App
555	272	10.8	463	16	US-10-215-371-285	Sequence 285, App
556	272	10.8	463	16	US-10-771-187-285	Sequence 285, App
557	272	10.8	463	17	US-10-931-886-360	Sequence 360, App
558	265	10.5	498	10	US-09-789-390-21	Sequence 21, Appl
559	265	10.5	498	10	US-09-789-390-76	Sequence 76, Appl
607	260.5	10.3	497	14	US-10-219-065-56	Sequence 56, Appl
662	260.5	10.3	497	15	US-10-416-314-63	Sequence 63, Appl
664	259.5	10.3	497	10	US-09-789-390-17	Sequence 17, Appl
665	257.5	10.2	468	10	US-09-789-390-43	Sequence 43, Appl
666	257.5	10.2	497	10	US-09-789-390-44	Sequence 44, Appl
667	257.5	10.2	497	10	US-09-789-390-45	Sequence 45, Appl
668	256.5	10.1	468	10	US-09-789-390-75	Sequence 75, Appl
669	256.5	10.1	477	10	US-09-789-390-19	Sequence 19, Appl
670	254.5	10.1	239	14	US-10-091-135-85	Sequence 85, Appl
671	254.5	10.1	255	9	US-09-876-225-2	Sequence 2, Appli
672	254.5	10.1	255	15	US-10-417-727-2	Sequence 2, Appli
673	254.5	10.1	257	10	US-09-800-198-88	Sequence 88, Appl
674	254.5	10.1	258	9	US-09-808-602-110	Sequence 110, App
675	254.5	10.1	258	10	US-09-800-198-96	Sequence 96, Appl
676	254.5	10.1	258	15	US-10-058-270A-124	Sequence 124, App
677	254.5	10.1	258	16	US-10-755-889-402	Sequence 402, App
678	253	10.0	253	10	US-09-800-198-97	Sequence 97, Appl
679	253	10.0	253	15	US-10-243-552-580	Sequence 580, App
680	253	10.0	253	15	US-10-094-886-120	Sequence 120, App
681	252	10.0	191	10	US-09-789-390-42	Sequence 42, Appl
682	252	10.0	191	10	US-09-789-390-46	Sequence 46, Appl
683	252	10.0	245	14	US-10-205-823-363	Sequence 363, App
684	252	10.0	245	15	US-10-341-434-28	Sequence 28, Appl
685	252	10.0	245	15	US-10-341-434-45	Sequence 45, Appl
686	250	9.9	245	10	US-09-800-198-98	Sequence 98, Appl
1120	249	9.8	242	17	US-10-931-886-262	Sequence 262, App
1121	247.5	9.8	191	10	US-09-789-390-74	Sequence 74, Appl
1122	241	9.5	300	9	US-09-808-602-27	Sequence 27, Appl
1123	241	9.5	300	10	US-09-800-198-25	Sequence 25, Appl
1124	240	9.5	188	9	US-09-808-602-109	Sequence 109, App
1125	240	9.5	188	10	US-09-800-198-95	Sequence 95, Appl
1126	237.5	9.4	431	9	US-09-808-602-113	Sequence 113, App
1127	237.5	9.4	501	10	US-09-789-390-23	Sequence 23, Appl
1128	237.5	9.4	501	10	US-09-789-390-77	Sequence 77, Appl
1129	235.5	9.3	500	9	US-09-808-602-108	Sequence 108, App
1130	235.5	9.3	500	9	US-09-808-602-112	Sequence 112, App
1131	235.5	9.3	500	9	US-09-808-602-114	Sequence 114, App
1151	235.5	9.3	500	10	US-09-800-198-94	Sequence 94, Appl
1415	235.5	9.3	500	14	US-10-167-749-363	Sequence 363, App

Search completed: February 11, 2005, 19:22:51
Job time : 170 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 18:27:16 ; Search time 44 Seconds
(without alignments)
771.939 Million cell updates/sec

Title: US-09-943-664-50
Perfect score: 2529
Sequence: 1 MLHPETSPGRGHLLAVLLAL.....RNRYICQFAQEHISRWGPGS 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2529	100.0	455	4	US-09-866-028-50	Sequence 50, Appl
2	2529	100.0	455	4	US-09-944-457-50	Sequence 50, Appl
3	272	10.8	463	4	US-09-907-794A-285	Sequence 285, App
4	272	10.8	463	4	US-09-905-125A-285	Sequence 285, App
5	272	10.8	463	4	US-09-902-775A-285	Sequence 285, App
6	272	10.8	463	4	US-09-906-700-285	Sequence 285, App
7	272	10.8	463	4	US-09-903-603A-285	Sequence 285, App
8	272	10.8	463	4	US-09-904-920A-285	Sequence 285, App
9	272	10.8	463	4	US-09-909-064-285	Sequence 285, App
10	272	10.8	463	4	US-09-905-381A-285	Sequence 285, App
11	272	10.8	463	4	US-09-906-618-285	Sequence 285, App
12	267	10.6	270	2	US-08-773-368-1	Sequence 1, Appli
13	267	10.6	270	3	US-09-199-887-1	Sequence 1, Appli
14	259	10.2	258	4	US-09-698-781-3	Sequence 3, Appli
15	232	9.2	219	2	US-08-773-368-3	Sequence 3, Appli
16	232	9.2	219	3	US-09-199-887-3	Sequence 3, Appli
17	231	9.1	266	2	US-08-773-368-4	Sequence 4, Appli
18	231	9.1	266	3	US-09-199-887-4	Sequence 4, Appli
19	222.5	8.8	257	4	US-09-949-016-7490	Sequence 7490, Ap
20	221	8.7	243	4	US-09-541-759-7	Sequence 7, Appli
21	213.5	8.4	249	4	US-09-949-016-6025	Sequence 6025, Ap
22	213.5	8.4	267	4	US-09-949-016-7489	Sequence 7489, Ap
23	212	8.4	1257	1	US-08-340-428B-49	Sequence 49, Appl
24	196	7.8	2409	6	5180808-2	Patent No. 5180808
25	196	7.8	2409	6	5180808-2	Patent No. 5180808
26	189.5	7.5	1455	3	US-08-840-062-5	Sequence 5, Appli
27	185	7.3	151	1	US-08-614-935-28	Sequence 28, Appl
28	185	7.3	151	3	US-09-130-287-28	Sequence 28, Appl
29	182.5	7.2	135	2	US-07-857-224B-97	Sequence 97, Appl
30	182.5	7.2	135	2	US-07-857-224B-98	Sequence 98, Appl
31	180.5	7.1	135	2	US-07-857-224B-99	Sequence 99, Appl
32	180.5	7.1	205	1	US-08-419-414-10	Sequence 10, Appl
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34	180.5	7.1	205	1	US-08-614-935-7	Sequence 7, Appli
35	180.5	7.1	205	3	US-09-130-287-6	Sequence 6, Appli
36	180.5	7.1	205	3	US-09-130-287-7	Sequence 7, Appli
37	178.5	7.1	1456	4	US-09-976-594-168	Sequence 168, App
38	178	7.0	737	4	US-09-866-028-15	Sequence 15, Appl
39	178	7.0	737	4	US-09-944-457-15	Sequence 15, Appl
40	174	6.9	111	2	US-07-857-224B-105	Sequence 105, App
41	172	6.8	138	2	US-07-857-224B-100	Sequence 100, App
42	172	6.8	163	4	US-09-257-583-13	Sequence 13, Appl
43	171	6.8	139	2	US-07-857-224B-101	Sequence 101, App
44	171	6.8	168	1	US-08-181-271A-45	Sequence 45, Appl
45	171	6.8	168	1	US-08-449-315-45	Sequence 45, Appl
46	171	6.8	168	1	US-08-444-803-45	Sequence 45, Appl
47	171	6.8	168	1	US-08-449-043-45	Sequence 45, Appl
48	171	6.8	168	1	US-08-456-265A-45	Sequence 45, Appl
49	171	6.8	168	1	US-08-455-416-45	Sequence 45, Appl
50	171	6.8	168	1	US-08-455-244-45	Sequence 45, Appl
51	171	6.8	168	1	US-08-454-876-45	Sequence 45, Appl
52	171	6.8	168	2	US-08-457-364-45	Sequence 45, Appl
53	171	6.8	168	2	US-08-456-262-45	Sequence 45, Appl
54	171	6.8	168	2	US-08-456-240-45	Sequence 45, Appl
55	171	6.8	168	2	US-08-455-736-45	Sequence 45, Appl
56	171	6.8	168	2	US-08-971-217-45	Sequence 45, Appl
57	171	6.8	168	3	US-09-350-600-45	Sequence 45, Appl
58	171	6.8	168	4	US-09-906-234-45	Sequence 45, Appl
59	169	6.7	204	1	US-08-614-935-1	Sequence 1, Appli
60	169	6.7	204	3	US-09-130-287-1	Sequence 1, Appli
61	168.5	6.7	912	5	PCT-US95-03747-2	Sequence 2, Appli
62	168.5	6.7	2321	4	US-09-230-652-2	Sequence 2, Appli
63	168	6.6	171	2	US-08-773-368-6	Sequence 6, Appli
64	168	6.6	171	3	US-09-199-887-6	Sequence 6, Appli
65	166	6.6	204	1	US-08-419-414-9	Sequence 9, Appli
66	166	6.6	204	1	US-08-614-935-2	Sequence 2, Appli
67	166	6.6	204	3	US-09-130-287-2	Sequence 2, Appli
68	166	6.6	227	4	US-09-541-759-6	Sequence 6, Appli
69	165	6.5	139	2	US-07-857-224B-102	Sequence 102, App
70	164.5	6.5	167	2	US-08-773-368-5	Sequence 5, Appli
71	164.5	6.5	167	3	US-09-199-887-5	Sequence 5, Appli
72	161.5	6.4	114	2	US-07-857-224B-106	Sequence 106, App
73	161.5	6.4	114	2	US-07-857-224B-108	Sequence 108, App
74	161.5	6.4	205	1	US-08-614-935-4	Sequence 4, Appli
75	161.5	6.4	205	3	US-09-130-287-4	Sequence 4, Appli
76	161.5	6.4	2523	1	US-08-185-432-18	Sequence 18, Appl
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78	161.5	6.4	2523	4	US-09-121-457-3	Sequence 3, Appli
79	161	6.4	273	4	US-09-638-203-2	Sequence 2, Appli
80	159	6.3	722	3	US-08-981-392-12	Sequence 12, Appl
81	159	6.3	722	4	US-09-908-322-12	Sequence 12, Appl
82	158.5	6.3	150	1	US-08-614-935-29	Sequence 29, Appl
83	158.5	6.3	150	3	US-09-130-287-29	Sequence 29, Appl
84	158.5	6.3	728	3	US-08-981-392-2	Sequence 2, Appli
85	158.5	6.3	728	4	US-09-908-322-2	Sequence 2, Appli
86	158.5	6.3	729	3	US-08-872-855-8	Sequence 8, Appli
87	158	6.2	424	1	US-08-419-414-2	Sequence 2, Appli
88	158	6.2	720	3	US-08-872-855-4	Sequence 4, Appli
89	157	6.2	204	1	US-08-614-935-5	Sequence 5, Appli
90	157	6.2	204	3	US-09-130-287-5	Sequence 5, Appli
91	156	6.2	520	3	US-09-068-740A-3	Sequence 3, Appli
92	156	6.2	702	3	US-09-068-740A-4	Sequence 4, Appli
93	156	6.2	723	3	US-09-068-740A-9	Sequence 9, Appli
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96	156	6.2	2703	1	US-08-185-432-19	Sequence 19, Appl
97	156	6.2	2703	4	US-08-899-232-4	Sequence 4, Appli
98	156	6.2	2703	4	US-09-121-457-4	Sequence 4, Appli
99	155	6.1	717	3	US-08-872-855-9	Sequence 9, Appli
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102	154.5	6.1	721	3	US-08-981-392-5	Sequence 5, Appli
103	154.5	6.1	721	4	US-09-908-322-5	Sequence 5, Appli
104	154	6.1	135	2	US-07-857-224B-103	Sequence 103, App
105	154	6.1	713	3	US-08-872-855-5	Sequence 5, Appli
106	153.5	6.1	721	3	US-08-872-855-7	Sequence 7, Appli
107	153	6.0	138	2	US-07-857-224B-112	Sequence 112, App
108	153	6.0	166	1	US-08-614-935-30	Sequence 30, Appl
109	153	6.0	166	3	US-09-130-287-30	Sequence 30, Appl
110	153	6.0	374	4	US-09-489-847-166	Sequence 166, App
111	152.5	6.0	134	4	US-09-621-976-3902	Sequence 3902, Ap
112	151	6.0	260	4	US-09-638-203-3	Sequence 3, Appli
113	150.5	6.0	1193	2	US-08-400-159-10	Sequence 10, Appl
114	150.5	6.0	1193	3	US-08-611-729A-10	Sequence 10, Appl
115	150.5	6.0	1193	4	US-09-195-524-10	Sequence 10, Appl
116	150.5	6.0	2254	4	US-09-949-016-9270	Sequence 9270, Ap
117	150	5.9	2471	1	US-08-185-432-16	Sequence 16, Appl
118	150	5.9	2471	1	US-08-083-590A-19	Sequence 19, Appl
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121	150	5.9	2471	4	US-09-121-457-1	Sequence 1, Appli
122	149.5	5.9	382	4	US-09-907-794A-137	Sequence 137, App
123	149.5	5.9	382	4	US-09-905-125A-137	Sequence 137, App
124	149.5	5.9	382	4	US-09-902-775A-137	Sequence 137, App
125	149.5	5.9	382	4	US-09-906-700-137	Sequence 137, App
126	149.5	5.9	382	4	US-09-903-603A-137	Sequence 137, App
127	149.5	5.9	382	4	US-09-904-920A-137	Sequence 137, App
128	149.5	5.9	382	4	US-09-909-064-137	Sequence 137, App
129	149.5	5.9	382	4	US-09-905-381A-137	Sequence 137, App
130	149.5	5.9	382	4	US-09-906-618-137	Sequence 137, App
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135	146	5.8	1010	3	US-08-882-046-7	Sequence 7, Appli
136	146	5.8	1010	4	US-09-566-047-7	Sequence 7, Appli
137	146	5.8	1036	3	US-09-068-740A-6	Sequence 6, Appli
138	146	5.8	1067	4	US-09-579-536C-18	Sequence 18, Appl
139	146	5.8	1187	3	US-09-068-740A-7	Sequence 7, Appli
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141	146	5.8	1208	4	US-10-213-329-1	Sequence 1, Appli
142	146	5.8	1218	2	US-08-400-159-6	Sequence 6, Appli
143	146	5.8	1218	3	US-08-611-729A-6	Sequence 6, Appli
144	146	5.8	1218	3	US-08-882-046-2	Sequence 2, Appli
145	146	5.8	1218	3	US-09-214-278-7	Sequence 7, Appli
146	146	5.8	1218	3	US-09-068-740A-11	Sequence 11, Appl
147	146	5.8	1218	4	US-09-855-722-7	Sequence 7, Appli
148	146	5.8	1218	4	US-09-566-047-2	Sequence 2, Appli
149	146	5.8	1218	4	US-09-917-254-85	Sequence 85, Appl
150	146	5.8	1218	4	US-09-195-524-6	Sequence 6, Appli
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152	146	5.8	1218	4	US-09-949-016-5902	Sequence 5902, Ap
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156	146	5.8	2556	4	US-09-121-457-2	Sequence 2, Appli
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159	144	5.7	1139	3	US-09-113-825-4	Sequence 4, Appli
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161	144	5.7	2556	3	US-08-532-384-20	Sequence 20, Appl
162	143.5	5.7	440	1	US-07-930-686-12	Sequence 12, Appl
163	143.5	5.7	440	2	US-08-460-998-12	Sequence 12, Appl
164	143.5	5.7	1248	3	US-08-882-046-6	Sequence 6, Appli
165	143.5	5.7	1248	4	US-09-566-047-6	Sequence 6, Appli
166	142.5	5.6	1480	3	US-09-182-024A-5	Sequence 5, Appli
167	142	5.6	203	1	US-08-419-414-8	Sequence 8, Appli
168	142	5.6	203	1	US-08-614-935-3	Sequence 3, Appli
169	142	5.6	203	3	US-09-130-287-3	Sequence 3, Appli
170	141	5.6	202	1	US-08-469-486-56	Sequence 56, Appl
171	141	5.6	202	2	US-08-469-658-56	Sequence 56, Appl
172	141	5.6	233	4	US-09-216-393B-110	Sequence 110, App
173	141	5.6	500	4	US-09-423-753-2	Sequence 2, Appli
174	141	5.6	659	4	US-09-423-753-3	Sequence 3, Appli
175	141	5.6	685	3	US-08-872-855-2	Sequence 2, Appli
176	141	5.6	685	4	US-09-423-753-25	Sequence 25, Appl
177	141	5.6	685	4	US-09-641-612-7	Sequence 7, Appli
178	141	5.6	1157	4	US-09-949-016-9568	Sequence 9568, Ap
179	141	5.6	1219	3	US-08-882-046-5	Sequence 5, Appli
180	141	5.6	1219	4	US-09-566-047-5	Sequence 5, Appli
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183	139.5	5.5	1065	2	US-08-400-159-8	Sequence 8, Appli
184	138.5	5.5	1148	3	US-08-882-046-4	Sequence 4, Appli
185	138.5	5.5	1148	4	US-09-566-047-4	Sequence 4, Appli
186	138	5.5	202	4	US-10-000-489-62	Sequence 62, Appl
187	137.5	5.4	272	4	US-09-949-016-9961	Sequence 9961, Ap
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189	137.5	5.4	287	4	US-09-862-802A-6	Sequence 6, Appli
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193	137.5	5.4	1055	4	US-09-855-722-2	Sequence 2, Appli
194	137.5	5.4	1212	3	US-09-214-278-3	Sequence 3, Appli
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197	137.5	5.4	1238	4	US-09-855-722-5	Sequence 5, Appli
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199	137.5	5.4	1257	4	US-09-195-524-8	Sequence 8, Appli
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203	136	5.4	187	4	US-09-535-521-17	Sequence 17, Appl
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206	136	5.4	292	4	US-09-535-521-5	Sequence 5, Appli
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211	135.5	5.4	833	1	US-08-083-590A-2	Sequence 2, Appli
212	135.5	5.4	833	1	US-08-465-500-6	Sequence 6, Appli
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214	135.5	5.4	833	2	US-08-346-128-6	Sequence 6, Appli
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216	135.5	5.4	833	3	US-08-893-828-6	Sequence 6, Appli
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223	134.5	5.3	977	4	US-09-733-764-1	Sequence 1, Appli
224	134.5	5.3	1124	1	US-08-323-474-2	Sequence 2, Appli
225	134.5	5.3	1124	4	US-09-949-016-5946	Sequence 5946, Ap
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229	134.5	5.3	1480	3	US-09-540-153-7	Sequence 7, Appli
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235	133.5	5.3	832	3	US-08-981-392-6	Sequence 6, Appli
236	133.5	5.3	832	4	US-09-908-322-6	Sequence 6, Appli
237	133	5.3	115	6	5514582-18	Patent No. 5514582
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243	132.5	5.2	179	2	US-09-113-788-3	Sequence 3, Appli
244	132.5	5.2	179	3	US-09-113-789-9	Sequence 9, Appli
245	132.5	5.2	179	4	US-09-919-039-130	Sequence 130, App
246	132.5	5.2	179	4	US-09-949-016-6200	Sequence 6200, Ap

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250	131.5	5.2	1101	2	US-08-469-537A-96	Sequence 96, Appl
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252	131.5	5.2	2199	5	PCT-US95-11684-2	Sequence 2, Appli
253	131	5.2	383	1	US-08-597-545-2	Sequence 2, Appli
254	131	5.2	383	1	US-08-457-135-2	Sequence 2, Appli
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257	131	5.2	1529	4	US-09-312-283C-396	Sequence 396, App
258	131	5.2	1799	4	US-09-845-583A-6	Sequence 6, Appli
259	131	5.2	3594	4	US-09-911-842A-4	Sequence 4, Appli
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262	130.5	5.2	1064	1	US-08-537-210A-3	Sequence 3, Appli
263	130.5	5.2	1064	3	US-09-113-825-3	Sequence 3, Appli
264	130.5	5.2	1118	1	US-07-934-393B-2	Sequence 2, Appli
265	130.5	5.2	1118	1	US-08-278-089A-2	Sequence 2, Appli
266	130.5	5.2	1118	2	US-08-838-957A-2	Sequence 2, Appli
267	130.5	5.2	1122	1	US-08-278-089A-6	Sequence 6, Appli
268	130.5	5.2	1122	2	US-08-838-957A-6	Sequence 6, Appli
269	130.5	5.2	2200	4	US-09-796-575-2	Sequence 2, Appli
270	130	5.1	316	3	US-09-111-470-4	Sequence 4, Appli
271	130	5.1	316	4	US-09-862-802A-4	Sequence 4, Appli
272	129.5	5.1	125	2	US-07-857-224B-114	Sequence 114, App
273	129.5	5.1	137	2	US-07-857-224B-110	Sequence 110, App
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275	129.5	5.1	379	4	US-09-907-794A-4	Sequence 4, Appli
276	129.5	5.1	379	4	US-09-905-125A-4	Sequence 4, Appli
277	129.5	5.1	379	4	US-09-902-775A-4	Sequence 4, Appli
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279	129.5	5.1	379	4	US-09-903-603A-4	Sequence 4, Appli
280	129.5	5.1	379	4	US-09-904-920A-4	Sequence 4, Appli
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283	129.5	5.1	379	4	US-09-906-618-4	Sequence 4, Appli
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285	129.5	5.1	385	1	US-08-457-135-1	Sequence 1, Appli
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288	129.5	5.1	1810	5	PCT-US95-11684-4	Sequence 4, Appli
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290	129	5.1	111	6	5514582-11	Patent No. 5514582
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292	129	5.1	299	3	US-09-188-930-332	Sequence 332, App
293	129	5.1	299	4	US-09-312-283C-192	Sequence 192, App
294	129	5.1	299	4	US-09-312-283C-332	Sequence 332, App
295	129	5.1	1135	2	US-08-469-537A-97	Sequence 97, Appl
296	128.5	5.1	114	6	5514582-13	Patent No. 5514582
297	128.5	5.1	114	6	5514582-13	Patent No. 5514582
298	128.5	5.1	220	4	US-09-541-759-4	Sequence 4, Appli
299	128.5	5.1	1576	4	US-09-562-702A-24	Sequence 24, Appl
300	128.5	5.1	1576	4	US-09-561-818A-24	Sequence 24, Appl
301	128.5	5.1	1584	4	US-09-562-702A-28	Sequence 28, Appl
302	128.5	5.1	1609	4	US-09-562-702A-22	Sequence 22, Appl
303	128.5	5.1	1609	4	US-09-561-818A-22	Sequence 22, Appl
304	128.5	5.1	1609	4	US-09-538-092-900	Sequence 900, App
305	128.5	5.1	1617	4	US-09-562-702A-26	Sequence 26, Appl
306	128.5	5.1	3075	2	US-08-460-309-5	Sequence 5, Appli
307	128.5	5.1	3075	2	US-08-125-077-5	Sequence 5, Appli
308	128.5	5.1	3571	4	US-09-911-842A-2	Sequence 2, Appli
309	128	5.1	1572	4	US-09-562-702A-32	Sequence 32, Appl
310	128	5.1	1572	4	US-09-561-818A-28	Sequence 28, Appl
311	128	5.1	1605	4	US-09-562-702A-30	Sequence 30, Appl
312	128	5.1	1605	4	US-09-561-818A-26	Sequence 26, Appl
313	127.5	5.0	197	4	US-09-602-877A-99	Sequence 99, Appl
314	127.5	5.0	1193	4	US-09-949-016-10498	Sequence 10498, A
315	127.5	5.0	1198	3	US-09-245-041-131	Sequence 131, App
316	127.5	5.0	1198	3	US-09-794-236-3	Sequence 3, Appli
317	127.5	5.0	1198	4	US-09-358-055B-132	Sequence 132, App
318	127.5	5.0	1350	3	US-09-245-041-17	Sequence 17, Appl
319	127.5	5.0	1350	4	US-09-358-055B-17	Sequence 17, Appl
320	127.5	5.0	1350	4	US-09-893-238-17	Sequence 17, Appl
321	127.5	5.0	1429	3	US-09-245-041-130	Sequence 130, App
322	127.5	5.0	1429	4	US-09-358-055B-131	Sequence 131, App
323	127.5	5.0	2787	3	US-09-245-041-15	Sequence 15, Appl
324	127.5	5.0	2787	4	US-09-358-055B-15	Sequence 15, Appl
325	127.5	5.0	2787	4	US-09-893-238-15	Sequence 15, Appl
326	127	5.0	205	1	US-08-450-944-5	Sequence 5, Appli
327	127	5.0	205	5	PCT-US96-07709-5	Sequence 5, Appli
328	127	5.0	220	4	US-09-541-759-3	Sequence 3, Appli
329	127	5.0	221	1	US-08-450-944-2	Sequence 2, Appli
330	127	5.0	221	5	PCT-US96-07709-2	Sequence 2, Appli
331	127	5.0	292	4	US-09-248-796A-15095	Sequence 15095, A
332	126.5	5.0	125	3	US-08-722-126A-7	Sequence 7, Appli
333	126.5	5.0	125	5	PCT-US95-04258-7	Sequence 7, Appli
334	126.5	5.0	287	1	US-08-365-103B-4	Sequence 4, Appli
335	126.5	5.0	289	4	US-09-862-802A-13	Sequence 13, Appl
336	126.5	5.0	300	1	US-08-365-103B-6	Sequence 6, Appli
337	126.5	5.0	327	1	US-08-365-103B-2	Sequence 2, Appli
338	126.5	5.0	1404	2	US-08-400-159-2	Sequence 2, Appli
339	126.5	5.0	1404	3	US-08-611-729A-2	Sequence 2, Appli
340	126.5	5.0	1404	4	US-09-195-524-2	Sequence 2, Appli
341	126.5	5.0	4391	4	US-10-006-011A-2	Sequence 2, Appli
342	126	5.0	219	4	US-09-907-794A-377	Sequence 377, App
343	126	5.0	219	4	US-09-905-125A-377	Sequence 377, App
344	126	5.0	219	4	US-09-902-775A-377	Sequence 377, App
345	126	5.0	219	4	US-09-906-700-377	Sequence 377, App
346	126	5.0	219	4	US-09-903-603A-377	Sequence 377, App
347	126	5.0	219	4	US-09-904-920A-377	Sequence 377, App
348	126	5.0	219	4	US-09-909-064-377	Sequence 377, App
349	126	5.0	219	4	US-09-905-381A-377	Sequence 377, App
350	126	5.0	219	4	US-09-906-618-377	Sequence 377, App
351	126	5.0	583	4	US-09-641-612-2	Sequence 2, Appli
352	126	5.0	1487	3	US-08-840-062-7	Sequence 7, Appli
353	125	4.9	1463	1	US-08-220-603A-11	Sequence 11, Appl
354	124.5	4.9	1138	1	US-08-323-474-8	Sequence 8, Appli
355	124.5	4.9	1138	2	US-08-469-537A-98	Sequence 98, Appl
356	124.5	4.9	1138	2	US-08-220-240A-5	Sequence 5, Appli
357	124.5	4.9	1150	4	US-09-949-016-7769	Sequence 7769, Ap
358	124.5	4.9	4544	1	US-08-469-486-52	Sequence 52, Appl
359	124.5	4.9	4544	2	US-08-469-658-52	Sequence 52, Appl
360	124	4.9	177	1	US-08-181-271A-46	Sequence 46, Appl
361	124	4.9	177	1	US-08-449-315-46	Sequence 46, Appl
362	124	4.9	177	1	US-08-444-803-46	Sequence 46, Appl
363	124	4.9	177	1	US-08-449-043-46	Sequence 46, Appl
364	124	4.9	177	1	US-08-456-265A-46	Sequence 46, Appl
365	124	4.9	177	1	US-08-455-416-46	Sequence 46, Appl
366	124	4.9	177	1	US-08-455-244-46	Sequence 46, Appl
367	124	4.9	177	1	US-08-454-876-46	Sequence 46, Appl
368	124	4.9	177	2	US-08-457-364-46	Sequence 46, Appl
369	124	4.9	177	2	US-08-456-262-46	Sequence 46, Appl
370	124	4.9	177	2	US-08-456-240-46	Sequence 46, Appl
371	124	4.9	177	2	US-08-455-736-46	Sequence 46, Appl
372	124	4.9	177	2	US-08-971-217-46	Sequence 46, Appl
373	124	4.9	177	3	US-09-350-600-46	Sequence 46, Appl
374	124	4.9	177	4	US-09-906-234-46	Sequence 46, Appl
375	123.5	4.9	114	6	5514582-8	Patent No. 5514582
376	123.5	4.9	114	6	5514582-8	Patent No. 5514582
377	123.5	4.9	642	3	US-08-872-855-10	Sequence 10, Appl
378	123.5	4.9	1068	1	US-08-537-210A-2	Sequence 2, Appli
379	123.5	4.9	1068	3	US-09-113-825-2	Sequence 2, Appli
380	123.5	4.9	1358	1	US-08-404-665-4	Sequence 4, Appli
381	123.5	4.9	1358	1	US-08-404-671-4	Sequence 4, Appli
382	123.5	4.9	1358	1	US-08-404-781-4	Sequence 4, Appli
383	123	4.9	124	2	US-07-857-224B-113	Sequence 113, App
384	123	4.9	144	4	US-09-949-016-10685	Sequence 10685, A
385	123	4.9	166	4	US-09-949-016-6286	Sequence 6286, Ap
386	123	4.9	204	5	PCT-US96-07709-33	Sequence 33, Appl
387	123	4.9	220	5	PCT-US96-07709-30	Sequence 30, Appl
388	123	4.9	248	5	PCT-US96-07709-25	Sequence 25, Appl
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390	123	4.9	678	1	US-08-435-434-2	Sequence 2, Appli
391	123	4.9	678	1	US-08-435-436-2	Sequence 2, Appli
392	123	4.9	678	2	US-08-438-863-2	Sequence 2, Appli

393	123	4.9	678	2	US-08-438-864-2	Sequence 2, Appli
394	123	4.9	678	3	US-08-438-862-2	Sequence 2, Appli
395	123	4.9	678	3	US-08-628-747-2	Sequence 2, Appli
396	123	4.9	678	3	US-08-402-253-2	Sequence 2, Appli
397	123	4.9	678	3	US-08-443-866B-2	Sequence 2, Appli
398	123	4.9	1935	4	US-09-949-016-10403	Sequence 10403, A
399	122.5	4.8	329	4	US-09-248-796A-15096	Sequence 15096, A
400	122.5	4.8	383	4	US-09-142-027A-12	Sequence 12, Appl
401	122.5	4.8	585	4	US-09-641-612-5	Sequence 5, Appli
402	122.5	4.8	1015	1	US-08-537-210A-1	Sequence 1, Appli
403	122.5	4.8	1015	3	US-09-113-825-1	Sequence 1, Appli
404	122	4.8	1449	3	US-08-840-062-6	Sequence 6, Appli
405	122	4.8	1723	4	US-09-194-612A-31	Sequence 31, Appl
406	121.5	4.8	273	3	US-09-111-470-10	Sequence 10, Appl
407	121.5	4.8	273	4	US-09-862-802A-10	Sequence 10, Appl
408	121.5	4.8	292	2	US-08-688-342-4	Sequence 4, Appli
409	121.5	4.8	292	2	US-09-113-788-4	Sequence 4, Appli
410	121.5	4.8	292	4	US-09-862-802A-12	Sequence 12, Appl
411	121.5	4.8	735	3	US-09-191-647-9	Sequence 9, Appli
412	121.5	4.8	735	3	US-09-540-245A-9	Sequence 9, Appli
413	121.5	4.8	735	3	US-09-540-153-9	Sequence 9, Appli
414	121.5	4.8	2871	4	US-09-538-092-1076	Sequence 1076, Ap
415	121	4.8	166	2	US-08-729-103-4	Sequence 4, Appli
416	121	4.8	174	4	US-09-949-016-10686	Sequence 10686, A
417	121	4.8	243	3	US-09-191-647-14	Sequence 14, Appl
418	121	4.8	243	3	US-09-540-245A-14	Sequence 14, Appl
419	121	4.8	243	3	US-09-540-153-14	Sequence 14, Appl
420	121	4.8	404	3	US-09-517-605-2	Sequence 2, Appli
421	120.5	4.8	112	2	US-07-857-224B-109	Sequence 109, App
422	119.5	4.7	114	6	5514582-10	Patent No. 5514582
423	119.5	4.7	114	6	5514582-10	Patent No. 5514582
424	119	4.7	196	3	US-08-981-392-35	Sequence 35, Appl
425	119	4.7	196	4	US-09-908-322-35	Sequence 35, Appl
426	118.5	4.7	323	4	US-09-065-040-4	Sequence 4, Appli
427	118.5	4.7	323	4	US-09-949-016-6294	Sequence 6294, Ap
428	118.5	4.7	1260	3	US-09-245-041-2	Sequence 2, Appli
429	118.5	4.7	1260	4	US-09-358-055B-2	Sequence 2, Appli
430	118.5	4.7	1260	4	US-09-893-238-2	Sequence 2, Appli
431	118.5	4.7	2123	4	US-09-949-016-7517	Sequence 7517, Ap
432	118.5	4.7	3070	4	US-09-961-403-7	Sequence 7, Appli
433	118.5	4.7	3084	4	US-09-562-702A-12	Sequence 12, Appl
434	118.5	4.7	3088	4	US-09-562-702A-8	Sequence 8, Appli
435	118.5	4.7	3089	4	US-09-562-702A-4	Sequence 4, Appli
436	118.5	4.7	3106	4	US-09-562-702A-10	Sequence 10, Appl
437	118.5	4.7	3110	4	US-09-562-702A-2	Sequence 2, Appli
438	118.5	4.7	3110	4	US-09-562-702A-6	Sequence 6, Appli
439	118.5	4.7	3110	4	US-09-561-709B-7	Sequence 7, Appli
440	118.5	4.7	3110	4	US-09-917-254-86	Sequence 86, Appl
441	118.5	4.7	3110	4	US-09-949-016-5937	Sequence 5937, Ap
442	118.5	4.7	3111	2	US-08-460-309-4	Sequence 4, Appli
443	118.5	4.7	3111	2	US-08-125-077-4	Sequence 4, Appli
444	117.5	4.6	652	2	US-08-751-305-2	Sequence 2, Appli
445	117	4.6	214	4	US-09-257-583-15	Sequence 15, Appl
446	116.5	4.6	994	4	US-10-164-595-38	Sequence 38, Appl
447	116.5	4.6	1854	4	US-09-949-016-11625	Sequence 11625, A
448	116	4.6	174	1	US-07-641-971B-1	Sequence 1, Appli
449	116	4.6	174	1	US-07-781-248A-1	Sequence 1, Appli
450	116	4.6	320	1	US-08-365-103B-10	Sequence 10, Appl
451	116	4.6	321	1	US-08-365-103B-8	Sequence 8, Appli
452	115.5	4.6	131	2	US-08-650-598-3	Sequence 3, Appli
453	115.5	4.6	647	4	US-09-949-016-10272	Sequence 10272, A
454	115	4.5	1722	4	US-09-194-612A-1	Sequence 1, Appli
455	114.5	4.5	1326	4	US-09-949-016-6806	Sequence 6806, Ap
456	114.5	4.5	1339	4	US-09-949-016-10448	Sequence 10448, A
457	114.5	4.5	1478	4	US-09-949-016-8315	Sequence 8315, Ap
458	114	4.5	593	1	US-07-668-648-4	Sequence 4, Appli
459	114	4.5	593	2	US-08-429-998-4	Sequence 4, Appli
460	114	4.5	593	2	US-08-431-333-4	Sequence 4, Appli
461	114	4.5	593	5	PCT-US91-02321-4	Sequence 4, Appli
462	114	4.5	613	4	US-09-949-016-9775	Sequence 9775, Ap
463	114	4.5	799	1	US-08-054-077C-2	Sequence 2, Appli
464	114	4.5	1587	4	US-09-845-583A-10	Sequence 10, Appl
465	114	4.5	1587	4	US-09-561-709B-3	Sequence 3, Appli
466	113.5	4.5	215	1	US-08-312-870-5	Sequence 5, Appli
467	113.5	4.5	446	1	US-08-307-444A-5	Sequence 5, Appli
468	113.5	4.5	446	1	US-08-587-389-5	Sequence 5, Appli
469	113.5	4.5	456	1	US-08-307-444A-3	Sequence 3, Appli
470	113.5	4.5	456	1	US-08-307-444A-4	Sequence 4, Appli
471	113.5	4.5	456	1	US-08-587-389-3	Sequence 3, Appli
472	113.5	4.5	456	1	US-08-587-389-4	Sequence 4, Appli
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475	113.5	4.5	475	1	US-08-587-389-1	Sequence 1, Appli
476	113.5	4.5	475	1	US-08-587-389-2	Sequence 2, Appli
477	113.5	4.5	476	1	US-08-014-723-1	Sequence 1, Appli
478	113.5	4.5	476	1	US-08-014-723-2	Sequence 2, Appli
479	113.5	4.5	476	1	US-08-014-723-18	Sequence 18, Appl
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481	113.5	4.5	476	1	US-08-110-011A-2	Sequence 2, Appli
482	113.5	4.5	476	1	US-08-110-011A-18	Sequence 18, Appl
483	113.5	4.5	494	1	US-08-014-723-14	Sequence 14, Appl
484	113.5	4.5	494	1	US-08-014-723-16	Sequence 16, Appl
485	113.5	4.5	494	1	US-08-110-011A-14	Sequence 14, Appl
486	113.5	4.5	494	1	US-08-110-011A-16	Sequence 16, Appl
487	113.5	4.5	497	1	US-08-312-870-3	Sequence 3, Appli
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490	113.5	4.5	516	4	US-09-509-994-1	Sequence 1, Appli
491	113.5	4.5	516	4	US-09-509-994-2	Sequence 2, Appli
492	113.5	4.5	575	1	US-08-261-206A-59	Sequence 59, Appl
493	113.5	4.5	575	1	US-08-312-870-1	Sequence 1, Appli
494	113.5	4.5	575	4	US-09-880-484D-2	Sequence 2, Appli
495	113.5	4.5	575	4	US-10-438-648-2	Sequence 2, Appli
496	113.5	4.5	575	6	5466668-6	Patent No. 5466668
497	113.5	4.5	575	6	5466668-6	Patent No. 5466668
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499	113	4.5	276	4	US-09-908-322-43	Sequence 43, Appl
500	113	4.5	376	4	US-09-248-796A-15097	Sequence 15097, A
501	112.5	4.4	110	6	5514582-12	Patent No. 5514582
502	112.5	4.4	110	6	5514582-12	Patent No. 5514582
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504	112.5	4.4	810	3	US-09-055-699-34	Sequence 34, Appl
505	112.5	4.4	810	3	US-09-273-565-34	Sequence 34, Appl
506	112.5	4.4	810	3	US-09-565-538-34	Sequence 34, Appl
507	112.5	4.4	810	3	US-09-661-468-34	Sequence 34, Appl
508	112.5	4.4	810	4	US-09-976-165-34	Sequence 34, Appl
509	112	4.4	165	2	US-08-401-530A-7	Sequence 7, Appli
510	112	4.4	165	2	US-08-729-103-3	Sequence 3, Appli
511	112	4.4	165	2	US-08-709-662-7	Sequence 7, Appli
512	112	4.4	179	4	US-09-148-545-177	Sequence 177, App
513	112	4.4	192	3	US-08-981-392-65	Sequence 65, Appl
514	112	4.4	192	4	US-09-908-322-65	Sequence 65, Appl
515	112	4.4	716	4	US-09-312-283C-183	Sequence 183, App
516	112	4.4	771	3	US-09-188-930-183	Sequence 183, App
517	111.5	4.4	3647	4	US-09-949-016-10932	Sequence 10932, A
518	111	4.4	816	2	US-08-820-170A-37	Sequence 37, Appl
519	111	4.4	816	3	US-09-055-699-37	Sequence 37, Appl
520	111	4.4	816	3	US-09-273-565-37	Sequence 37, Appl
521	111	4.4	816	3	US-09-565-538-37	Sequence 37, Appl
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523	111	4.4	816	4	US-09-976-165-37	Sequence 37, Appl
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525	110.5	4.4	158	2	US-08-468-413-2	Sequence 2, Appli
526	110.5	4.4	158	3	US-09-162-508-2	Sequence 2, Appli
527	110.5	4.4	158	5	PCT-US95-07169-2	Sequence 2, Appli
528	110	4.3	157	3	US-08-981-392-68	Sequence 68, Appl
529	110	4.3	157	4	US-09-908-322-68	Sequence 68, Appl
530	110	4.3	375	4	US-09-600-932-29	Sequence 29, Appl
531	110	4.3	380	4	US-09-205-258-441	Sequence 441, App
532	110	4.3	1171	1	US-08-445-135-1	Sequence 1, Appli
533	110	4.3	1798	4	US-09-561-709B-11	Sequence 11, Appl
534	109.5	4.3	248	4	US-09-600-932-28	Sequence 28, Appl
535	109.5	4.3	248	4	US-09-949-016-6612	Sequence 6612, Ap
536	109.5	4.3	251	4	US-09-949-016-8481	Sequence 8481, Ap
537	109.5	4.3	251	4	US-09-949-016-9058	Sequence 9058, Ap
538	109.5	4.3	259	4	US-09-949-016-9059	Sequence 9059, Ap

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540	109.5	4.3	2211	4	US-10-096-961A-1	Sequence 1, Appli
541	109	4.3	593	3	US-08-991-862-17	Sequence 17, Appl
542	109	4.3	593	4	US-09-813-156-17	Sequence 17, Appl
543	109	4.3	593	4	US-09-456-886-17	Sequence 17, Appl
544	109	4.3	593	4	US-09-824-647-17	Sequence 17, Appl
545	109	4.3	784	4	US-09-949-016-9467	Sequence 9467, Ap
546	109	4.3	3460	3	US-09-334-220-1	Sequence 1, Appli
547	108.5	4.3	485	4	US-09-949-016-10882	Sequence 10882, A
548	108.5	4.3	700	4	US-08-933-711B-5	Sequence 5, Appli
549	108	4.3	495	4	US-10-006-011A-4	Sequence 4, Appli
550	108	4.3	705	4	US-10-006-011A-3	Sequence 3, Appli
551	107.5	4.3	178	4	US-09-706-722A-7	Sequence 7, Appli
552	107.5	4.3	577	2	US-07-728-215-29	Sequence 29, Appl
553	107.5	4.3	577	3	US-08-938-085A-29	Sequence 29, Appl
554	107.5	4.3	577	4	US-10-072-844-29	Sequence 29, Appl
555	107.5	4.3	577	4	US-10-072-838-29	Sequence 29, Appl
556	107.5	4.3	577	4	US-10-072-841A-29	Sequence 29, Appl
557	107.5	4.3	577	4	US-10-219-631A-29	Sequence 29, Appl
558	107.5	4.3	757	4	US-09-949-016-6963	Sequence 6963, Ap
559	107.5	4.3	758	4	US-09-949-016-8087	Sequence 8087, Ap
560	107.5	4.3	769	2	US-08-789-078-1	Sequence 1, Appli
561	107.5	4.3	769	2	US-08-752-633-1	Sequence 1, Appli
562	107.5	4.3	769	2	US-08-476-062A-45	Sequence 45, Appl
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564	107.5	4.3	769	3	US-08-938-085A-31	Sequence 31, Appl
565	107.5	4.3	769	4	US-10-072-844-31	Sequence 31, Appl
566	107.5	4.3	769	4	US-10-072-838-31	Sequence 31, Appl
567	107.5	4.3	769	4	US-10-072-841A-31	Sequence 31, Appl
568	107.5	4.3	769	4	US-10-219-631A-31	Sequence 31, Appl
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573	107	4.2	788	2	US-07-728-215-32	Sequence 32, Appl
574	107	4.2	788	3	US-08-938-085A-32	Sequence 32, Appl
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577	107	4.2	788	4	US-10-072-844-32	Sequence 32, Appl
578	107	4.2	788	4	US-10-072-838-32	Sequence 32, Appl
579	107	4.2	788	4	US-10-072-841A-32	Sequence 32, Appl
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581	107	4.2	788	4	US-09-054-272-44	Sequence 44, Appl
582	107	4.2	788	4	US-10-219-631A-32	Sequence 32, Appl
583	107	4.2	788	4	US-09-949-016-5901	Sequence 5901, Ap
584	106.5	4.2	157	3	US-08-872-855-6	Sequence 6, Appli
585	106.5	4.2	655	1	US-08-148-910-12	Sequence 12, Appl
586	106.5	4.2	655	1	US-08-448-937A-12	Sequence 12, Appl
587	106.5	4.2	700	4	US-08-933-711B-6	Sequence 6, Appli
588	106.5	4.2	999	4	US-09-747-371-2	Sequence 2, Appli
589	106	4.2	72	1	US-08-450-944-7	Sequence 7, Appli
590	106	4.2	72	5	PCT-US96-07709-7	Sequence 7, Appli
591	106	4.2	160	3	US-09-191-647-5	Sequence 5, Appli
592	106	4.2	160	3	US-09-540-245A-5	Sequence 5, Appli
593	106	4.2	160	3	US-09-540-153-5	Sequence 5, Appli
594	106	4.2	492	3	US-09-724-864-39	Sequence 39, Appl
595	106	4.2	1761	4	US-09-561-709B-1	Sequence 1, Appli
596	105.5	4.2	238	4	US-08-450-482B-117	Sequence 117, App
597	105.5	4.2	575	1	US-08-170-290A-54	Sequence 54, Appl
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599	105	4.2	197	4	US-09-370-838-206	Sequence 206, App
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601	105	4.2	227	4	US-08-450-482B-125	Sequence 125, App
602	105	4.2	229	4	US-08-450-482B-127	Sequence 127, App
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604	105	4.2	961	5	PCT-US93-11725-4	Sequence 4, Appli
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606	104.5	4.1	238	4	US-09-862-802A-8	Sequence 8, Appli
607	104.5	4.1	1656	4	US-09-949-016-7247	Sequence 7247, Ap
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609	104.5	4.1	1798	4	US-09-917-254-87	Sequence 87, Appl
610	104.5	4.1	1821	4	US-09-949-016-5938	Sequence 5938, Ap
611	104	4.1	194	3	US-09-188-930-335	Sequence 335, App
612	104	4.1	194	4	US-09-312-283C-335	Sequence 335, App
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616	104	4.1	908	4	US-08-714-741-44	Sequence 44, Appl
617	104	4.1	1725	4	US-09-560-385A-10	Sequence 10, Appl
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619	103.5	4.1	1111	1	US-08-317-450B-15	Sequence 15, Appl
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621	103.5	4.1	1172	4	US-09-560-385A-28	Sequence 28, Appl
622	103.5	4.1	1172	4	US-09-560-385A-32	Sequence 32, Appl
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626	103.5	4.1	1193	4	US-09-560-385A-30	Sequence 30, Appl
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628	103	4.1	122	5	PCT-US95-04258-9	Sequence 9, Appli
629	103	4.1	139	4	US-09-248-796A-15094	Sequence 15094, A
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632	103	4.1	638	4	US-09-482-273-245	Sequence 245, App
633	103	4.1	788	2	US-07-728-215-27	Sequence 27, Appl
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637	103	4.1	788	4	US-10-072-841A-27	Sequence 27, Appl
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645	102.5	4.1	351	4	US-09-358-055B-11	Sequence 11, Appl
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657	102.5	4.1	419	4	US-10-182-263-5	Sequence 5, Appli
658	102.5	4.1	419	4	US-10-182-263-6	Sequence 6, Appli
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693	102	4.0	790	4	US-09-949-016-8169	Sequence 8169, Ap
694	102	4.0	790	4	US-09-949-016-8170	Sequence 8170, Ap
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696	102	4.0	5405	3	US-08-718-388-9	Sequence 9, Appli
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698	101.5	4.0	448	3	US-09-212-168-1	Sequence 1, Appli
699	101.5	4.0	448	4	US-09-409-096-4	Sequence 4, Appli
700	101.5	4.0	504	4	US-09-949-016-7403	Sequence 7403, Ap
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705	101	4.0	320	3	US-09-022-765-55	Sequence 55, Appl
706	101	4.0	320	4	US-09-551-974A-22	Sequence 22, Appl
707	101	4.0	320	4	US-09-551-974A-55	Sequence 55, Appl
708	101	4.0	320	4	US-09-565-501A-22	Sequence 22, Appl
709	101	4.0	320	4	US-09-565-501A-55	Sequence 55, Appl
710	101	4.0	320	4	US-09-639-206A-22	Sequence 22, Appl
711	101	4.0	320	4	US-09-639-206A-55	Sequence 55, Appl
712	101	4.0	320	4	US-09-874-923-22	Sequence 22, Appl
713	101	4.0	320	4	US-09-874-923-55	Sequence 55, Appl
714	101	4.0	320	4	US-08-798-841-22	Sequence 22, Appl
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716	101	4.0	673	1	US-08-435-434-1	Sequence 1, Appli
717	101	4.0	673	1	US-08-435-436-1	Sequence 1, Appli
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720	101	4.0	673	3	US-08-438-862-1	Sequence 1, Appli
721	101	4.0	673	3	US-08-628-747-1	Sequence 1, Appli
722	101	4.0	673	3	US-08-402-253-1	Sequence 1, Appli
723	101	4.0	673	3	US-08-443-866B-1	Sequence 1, Appli
724	101	4.0	676	3	US-08-630-172-10	Sequence 10, Appl
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732	101	4.0	4302	4	US-09-052-262-8	Sequence 8, Appli
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753	99.5	3.9	242	4	US-08-981-799A-119	Sequence 119, App
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755	99.5	3.9	264	4	US-08-981-799A-115	Sequence 115, App
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770	99	3.9	610	6	5217870-2	Patent No. 5217870
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772	99	3.9	965	4	US-09-538-092-650	Sequence 650, App
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775	98.5	3.9	78	1	US-08-083-590A-15	Sequence 15, Appl
776	98.5	3.9	78	1	US-08-465-500-2	Sequence 2, Appli
777	98.5	3.9	78	2	US-08-346-126-2	Sequence 2, Appli
778	98.5	3.9	78	2	US-08-346-128-2	Sequence 2, Appli
779	98.5	3.9	78	3	US-08-532-384-15	Sequence 15, Appl
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782	98.5	3.9	174	2	US-08-709-662-6	Sequence 6, Appli
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793	98.5	3.9	387	2	US-08-833-963C-9	Sequence 9, Appli
794	98.5	3.9	387	3	US-08-980-514-3	Sequence 3, Appli
795	98.5	3.9	387	3	US-09-212-168-5	Sequence 5, Appli
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799	98.5	3.9	857	3	US-09-256-490-2	Sequence 2, Appli
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806	97.5	3.9	677	4	US-09-949-016-11369	Sequence 11369, A
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817	97.5	3.9	2088	4	US-09-548-373D-13	Sequence 13, Appl
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825	97	3.8	787	4	US-10-000-489-70	Sequence 70, Appl
826	97	3.8	799	2	US-08-525-940-23	Sequence 23, Appl
827	97	3.8	799	2	US-08-976-838-23	Sequence 23, Appl
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829	97	3.8	881	2	US-08-976-838-21	Sequence 21, Appl
830	97	3.8	915	2	US-08-525-940-18	Sequence 18, Appl

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833	97	3.8	915	3	US-09-214-555B-7	Sequence 7, Appli
834	97	3.8	1436	4	US-09-578-063-78	Sequence 78, Appl
835	97	3.8	1586	4	US-09-060-299-44	Sequence 44, Appl
836	97	3.8	1586	4	US-09-402-923A-44	Sequence 44, Appl
837	97	3.8	1614	4	US-09-060-299-42	Sequence 42, Appl
838	97	3.8	1614	4	US-09-402-923A-42	Sequence 42, Appl
839	97	3.8	1882	3	US-09-369-364A-13	Sequence 13, Appl
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841	96.5	3.8	291	2	US-08-688-342-5	Sequence 5, Appli
842	96.5	3.8	291	2	US-09-113-788-5	Sequence 5, Appli
843	96.5	3.8	291	3	US-09-111-470-5	Sequence 5, Appli
844	96.5	3.8	291	4	US-09-862-802A-5	Sequence 5, Appli
845	96.5	3.8	296	4	US-09-489-847-293	Sequence 293, App
846	96.5	3.8	311	4	US-09-949-016-9962	Sequence 9962, Ap
847	96.5	3.8	335	4	US-09-312-283C-186	Sequence 186, App
848	96.5	3.8	347	4	US-09-636-215-590	Sequence 590, App
849	96.5	3.8	347	4	US-09-685-166A-590	Sequence 590, App
850	96.5	3.8	347	4	US-09-679-426-590	Sequence 590, App
851	96.5	3.8	347	4	US-09-759-143-590	Sequence 590, App
852	96.5	3.8	347	4	US-09-651-236-590	Sequence 590, App
853	96.5	3.8	374	2	US-08-820-170A-25	Sequence 25, Appl
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855	96.5	3.8	374	3	US-09-273-565-25	Sequence 25, Appl
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857	96.5	3.8	374	3	US-09-661-468-25	Sequence 25, Appl
858	96.5	3.8	374	4	US-09-976-165-25	Sequence 25, Appl
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860	96.5	3.8	374	5	PCT-US95-06385-2	Sequence 2, Appli
861	96.5	3.8	482	4	US-08-933-711B-8	Sequence 8, Appli
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868	96.5	3.8	1497	4	US-09-060-854B-2	Sequence 2, Appli
869	96.5	3.8	1497	4	US-09-529-904-3	Sequence 3, Appli
870	96.5	3.8	1621	4	US-09-949-016-8450	Sequence 8450, Ap
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875	96	3.8	237	4	US-09-862-802A-2	Sequence 2, Appli
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877	96	3.8	915	4	US-09-907-794A-34	Sequence 34, Appl
878	96	3.8	915	4	US-09-905-125A-34	Sequence 34, Appl
879	96	3.8	915	4	US-09-902-775A-34	Sequence 34, Appl
880	96	3.8	915	4	US-09-906-700-34	Sequence 34, Appl
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882	96	3.8	915	4	US-09-904-920A-34	Sequence 34, Appl
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884	96	3.8	915	4	US-09-905-381A-34	Sequence 34, Appl
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888	96	3.8	1786	4	US-09-562-702A-18	Sequence 18, Appl
889	96	3.8	1786	4	US-09-561-818A-18	Sequence 18, Appl
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898	95.5	3.8	317	4	US-09-823-038A-20	Sequence 20, Appl
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900	95.5	3.8	351	3	US-09-029-156-1	Sequence 1, Appli
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904	95.5	3.8	846	4	US-10-072-838-33	Sequence 33, Appl
905	95.5	3.8	846	4	US-10-072-841A-33	Sequence 33, Appl
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908	95.5	3.8	956	4	US-09-949-016-6215	Sequence 6215, Ap
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910	95.5	3.8	2594	3	US-08-718-388-7	Sequence 7, Appli
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916	95	3.8	350	2	US-08-824-996-2	Sequence 2, Appli
917	95	3.8	350	3	US-09-042-105-4	Sequence 4, Appli
918	95	3.8	350	3	US-08-510-133A-33	Sequence 33, Appl
919	95	3.8	350	3	US-08-585-895-33	Sequence 33, Appl
920	95	3.8	350	4	US-10-084-488-4	Sequence 4, Appli
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922	95	3.8	419	3	US-09-042-105-2	Sequence 2, Appli
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926	95	3.8	419	3	US-09-355-700-8	Sequence 8, Appli
927	95	3.8	419	3	US-09-355-700-58	Sequence 58, Appl
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931	95	3.8	419	4	US-08-465-968-2	Sequence 2, Appli
932	95	3.8	419	4	US-08-671-573B-33	Sequence 33, Appl
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934	95	3.8	419	4	US-09-631-092B-33	Sequence 33, Appl
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938	95	3.8	419	4	US-09-468-647A-108	Sequence 108, App
939	95	3.8	419	4	US-09-534-376A-8	Sequence 8, Appli
940	95	3.8	419	4	US-09-534-376A-58	Sequence 58, Appl
941	95	3.8	419	4	US-09-169-079-21	Sequence 21, Appl
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944	95	3.8	465	2	US-08-162-402B-8	Sequence 8, Appli
945	95	3.8	486	4	US-09-914-259-35	Sequence 35, Appl
946	95	3.8	486	4	US-09-976-594-278	Sequence 278, App
947	95	3.8	486	4	US-09-949-016-6216	Sequence 6216, Ap
948	95	3.8	507	4	US-09-949-016-9878	Sequence 9878, Ap
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952	94.5	3.7	175	2	US-08-709-662-3	Sequence 3, Appli
953	94.5	3.7	248	4	US-08-450-482B-115	Sequence 115, App
954	94.5	3.7	513	2	US-08-480-229C-14	Sequence 14, Appl
955	94.5	3.7	513	2	US-08-659-235C-14	Sequence 14, Appl
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957	94.5	3.7	584	4	US-09-949-016-10341	Sequence 10341, A
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962	94	3.7	686	4	US-09-358-055B-13	Sequence 13, Appl
963	94	3.7	686	4	US-09-893-238-13	Sequence 13, Appl
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965	94	3.7	1153	4	US-09-560-385A-16	Sequence 16, Appl
966	94	3.7	1170	4	US-09-561-709B-12	Sequence 12, Appl
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969	94	3.7	1196	2	US-08-735-893-4	Sequence 4, Appli
970	94	3.7	1765	4	US-09-562-702A-16	Sequence 16, Appl
971	94	3.7	1765	4	US-09-561-818A-16	Sequence 16, Appl
972	94	3.7	1786	4	US-09-562-702A-14	Sequence 14, Appl
973	94	3.7	1786	4	US-09-561-818A-14	Sequence 14, Appl
974	94	3.7	1786	4	US-09-561-709B-9	Sequence 9, Appli
975	94	3.7	1786	4	US-09-538-092-869	Sequence 869, App
976	93.5	3.7	461	3	US-08-742-877-2	Sequence 2, Appli

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980	93.5	3.7	589	2	US-08-429-998-6	Sequence 6, Appli
981	93.5	3.7	589	2	US-08-431-333-6	Sequence 6, Appli
982	93.5	3.7	589	3	US-08-991-862-2	Sequence 2, Appli
983	93.5	3.7	589	4	US-09-813-156-2	Sequence 2, Appli
984	93.5	3.7	589	4	US-09-456-886-2	Sequence 2, Appli
985	93.5	3.7	589	4	US-09-824-647-2	Sequence 2, Appli
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988	93.5	3.7	1083	2	US-08-596-405-2	Sequence 2, Appli
989	93.5	3.7	1083	2	US-08-877-620-2	Sequence 2, Appli
990	93.5	3.7	1083	4	US-09-287-368-2	Sequence 2, Appli
991	93.5	3.7	1083	4	US-09-626-795-2	Sequence 2, Appli
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993	93.5	3.7	1917	4	US-09-627-650B-5	Sequence 5, Appli
994	93.5	3.7	1917	4	US-09-436-063C-5	Sequence 5, Appli
995	93.5	3.7	2813	4	US-09-381-261A-1	Sequence 1, Appli
996	93.5	3.7	4654	3	US-08-476-515A-84	Sequence 84, Appl
997	93.5	3.7	4655	3	US-08-652-877-84	Sequence 84, Appl
998	93.5	3.7	4655	3	US-08-652-877-86	Sequence 86, Appl
999	93.5	3.7	4655	3	US-08-652-877-88	Sequence 88, Appl
1000	93.5	3.7	4655	3	US-08-652-877-90	Sequence 90, Appl
1001	93	3.7	120	1	US-08-274-661B-36	Sequence 36, Appl
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1004	93	3.7	216	3	US-08-543-246B-24	Sequence 24, Appl
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1008	93	3.7	589	5	PCT-US91-02321-2	Sequence 2, Appli
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1028	92.5	3.7	1019	2	US-08-596-405-4	Sequence 4, Appli
1029	92.5	3.7	1019	2	US-08-877-620-4	Sequence 4, Appli
1030	92.5	3.7	1019	4	US-09-287-368-4	Sequence 4, Appli
1031	92.5	3.7	1019	4	US-09-626-795-4	Sequence 4, Appli
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1037	92	3.6	174	2	US-08-709-662-2	Sequence 2, Appli
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1043	92	3.6	492	4	US-09-986-552-19	Sequence 19, Appl
1044	92	3.6	492	4	US-09-636-596C-19	Sequence 19, Appl
1045	92	3.6	492	4	US-10-023-894-20	Sequence 20, Appl
1046	92	3.6	492	4	US-10-306-686-19	Sequence 19, Appl
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1051	91.5	3.6	192	4	US-09-252-991A-22703	Sequence 22703, A
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1059	91.5	3.6	415	2	US-08-955-471-2	Sequence 2, Appli
1060	91.5	3.6	415	2	US-08-766-288-1	Sequence 1, Appli
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1062	91.5	3.6	443	2	US-08-833-963C-2	Sequence 2, Appli
1063	91.5	3.6	443	3	US-08-980-514-1	Sequence 1, Appli
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1078	91	3.6	1172	4	US-09-919-172-16	Sequence 16, Appl
1079	91	3.6	1174	4	US-09-560-385A-22	Sequence 22, Appl
1080	91	3.6	1186	4	US-09-560-385A-18	Sequence 18, Appl
1081	91	3.6	1345	2	US-08-977-767-3	Sequence 3, Appli
1082	91	3.6	3461	3	US-09-334-220-2	Sequence 2, Appli
1083	90.5	3.6	77	4	US-09-531-056A-22	Sequence 22, Appl
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1085	90.5	3.6	559	4	US-10-136-227A-28	Sequence 28, Appl
1086	90.5	3.6	559	4	US-09-981-649A-28	Sequence 28, Appl
1087	90.5	3.6	620	1	US-08-325-071-65	Sequence 65, Appl
1088	90.5	3.6	620	3	US-08-461-004A-65	Sequence 65, Appl
1089	90.5	3.6	943	3	US-08-476-515A-12	Sequence 12, Appl
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1487	82	3.2	1245	4	US-09-367-764-6	Sequence 6, Appli
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ALIGNMENTS

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RESULT 1
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; Sequence 50, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/866,028
;  CURRENT FILING DATE:  2001-05-25
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 50
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-866-028-50

  Query Match           100.0%;  Score 2529;  DB 4;  Length 455;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-218;
  Matches  455;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
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; Sequence 50, Application US/09944457
; Patent No. 6734288
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin
;  APPLICANT:  Botstein,David
;  APPLICANT:  Eaton,Dan
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul
;  APPLICANT:  Grimaldi,Christopher
;  APPLICANT:  Gurney,Austin
;  APPLICANT:  Hillan,Kenneth
;  APPLICANT:  Kljavin,Ivar
;  APPLICANT:  Napier,Mary
;  APPLICANT:  Roy,Margaret
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Wood,William
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P2548P1C1
;  CURRENT APPLICATION NUMBER: US/09/944,457
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: 09/866,028
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/067,411
;  PRIOR FILING DATE: December 3, 1997
;  PRIOR APPLICATION NUMBER: 60/069,334
;  PRIOR FILING DATE: December 11, 1997
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;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,278
;  PRIOR FILING DATE: December 11, 1997
;  PRIOR APPLICATION NUMBER: 60/069,425
;  PRIOR FILING DATE: December 12, 1997
;  PRIOR APPLICATION NUMBER: 60/069,696
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,694
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,702
;  PRIOR FILING DATE: December 16, 1997
;  PRIOR APPLICATION NUMBER: 60/069,870
;  PRIOR FILING DATE: December 17, 1997
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;  PRIOR FILING DATE: December 17, 1997
;  PRIOR APPLICATION NUMBER: 60/068,017
;  PRIOR FILING DATE: December 18, 1997
;  PRIOR APPLICATION NUMBER: 60/070,440
;  PRIOR FILING DATE: January 5, 1998
;  PRIOR APPLICATION NUMBER: 60/074,086
;  PRIOR FILING DATE: February 9, 1998
;  PRIOR APPLICATION NUMBER: 60/074,092
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;  PRIOR APPLICATION NUMBER: 60/075,945
;  PRIOR FILING DATE: February 25, 1998
;  PRIOR APPLICATION NUMBER: 60/112,850
;  PRIOR FILING DATE: December 16, 1998
;  PRIOR APPLICATION NUMBER: 60/113,296
;  PRIOR FILING DATE: December 22, 1998
;  PRIOR APPLICATION NUMBER: 60/146,222
;  PRIOR FILING DATE: July 28, 1999
;  PRIOR APPLICATION NUMBER: PCT/US98/19330
;  PRIOR FILING DATE: September 16, 1998
;  PRIOR APPLICATION NUMBER: PCT/US98/25108
;  PRIOR FILING DATE: December 1, 1998
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;  PRIOR APPLICATION NUMBER: 09/218,517
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;  PRIOR APPLICATION NUMBER: 09/254,311
;  PRIOR FILING DATE: March 3, 1999
;  PRIOR APPLICATION NUMBER: PCT/US99/12252
;  PRIOR FILING DATE: June 22, 1999
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;  PRIOR FILING DATE: September 15, 1999
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;  PRIOR FILING DATE: February 11, 2000
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;  PRIOR FILING DATE: February 22, 2000
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;  PRIOR FILING DATE: March 2, 2000
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;  PRIOR FILING DATE: March 30, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/14042
;  PRIOR FILING DATE: May 22, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/20710
;  PRIOR FILING DATE: July 28, 2000
;  PRIOR APPLICATION NUMBER: PCT/US00/32678
;  PRIOR FILING DATE: December 1, 2000
;  PRIOR APPLICATION NUMBER: PCT/US01/06520
;  PRIOR FILING DATE: February 28, 2001
;  NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 50
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-944-457-50

  Query Match           100.0%;  Score 2529;  DB 4;  Length 455;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-218;
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Qy          1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
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Db          1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60

Qy         61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120

Qy        121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180

Qy        181 AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240

Qy        241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300

Qy        301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT 360

Qy        361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420

Qy        421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
              ||||||||||||||||||||||||||||||||||
Db        421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
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RESULT 3
US-09-907-794A-285
; Sequence 285, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-794A-285

Query Match 10.8%; Score 272; DB 4; Length 463;
Best Local Similarity 31.9%; Pred. No. 5e-16;
Matches 74; Conservative 28; Mismatches 78; Indels 52; Gaps 9;

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Qy         13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRL 72
              || :|| |: ||             |: |||  :|  |:: |||  |: | | |:||  :
Db         11 LLPLLLLLVATT-----------GPV-GALTDEEKRLMVELHNLYRAQVSPTASDMLHM 57

Qy         73 DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV---------EV 123
               | : ||  |:| | |          :|     | | :    |   |
Db         58 RWDEELAAFAKAYARQC----------VW-----GHNKERGRRGENLFAITDEGMDVPLA 102

Qy        124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC----SAGQTAIEAFV 179
              :  |  | : |: :|  |:    | ||||:||| : ::||| | |       :| ||  |
Db        103 MEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLV 162

Qy        180 CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
              | | | ||  | ||   ||::|  || | :       :     |||   :|
Db        163 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-------GYHCKNSLCEPIGSP 203
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RESULT 4
US-09-905-125A-285
; Sequence 285, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14

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;  CURRENT APPLICATION NUMBER: US/09/905,125A
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-905-125A-285

  Query Match             10.8%;  Score 272;  DB 4;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 5e-16;
  Matches   74;  Conservative   28;  Mismatches   78;  Indels   52;  Gaps    9;

Qy         13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRL 72
              || :|| |: ||              |: |||  :|  |:: |||  |: | | |:||  :
Db         11 LLPLLLLLVATT------------GPV-GALTDEEKRLMVELHNLYRAQVSPTASDMLHM 57

Qy         73 DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV---------EV 123
               | : ||  |:| |  |           :|     | | :    |   |
Db         58 RWDEELAAFAKAYARQC----------VW-----GHNKERGRRGENLFAITDEGMDVPLA 102

Qy        124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC----SAGQTAIEAFV 179
              :  |  | : |: :|  |:    | ||||:||| : ::||| | |       :| ||  |
Db        103 MEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLV 162

Qy        180 CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
              | | | ||  | ||   ||::|  || | :      :     |||   :|
Db        163 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-------GYHCKNSLCEPIGSP 203


RESULT 5
US-09-902-775A-285
; Sequence 285, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,775A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-902-775A-285

  Query Match             10.8%;  Score 272;  DB 4;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 5e-16;
  Matches   74;  Conservative   28;  Mismatches   78;  Indels   52;  Gaps    9;

Qy         13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRL 72
              || :|| |: ||              |: |||  :|  |:: |||  |: | | |:||  :
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Db          11 LLPLLLLLVATT------------GPV-GALTDEEKRLMVELHNLYRAQVSPTASDMLHM 57

Qy          73 DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV---------EV 123
               | : ||  |:| |  |           :|     | | :     |   |
Db          58 RWDEELAAFAKAYARQC----------VW-----GHNKERGRRGENLFAITDEGMDVPLA 102

Qy         124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC----SAGQTAIEAFV 179
               :  |  | : |: :|  |:    | ||||:||| : ::||| | |          :| ||  |
Db         103 MEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLV 162

Qy         180 CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
               | | | ||  | ||   ||::|  || | :        :     |||   :|
Db         163 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-------GYHCKNSLCEPIGSP 203


RESULT 6
US-09-906-700-285
; Sequence 285, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,700
;  CURRENT FILING DATE:  2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-906-700-285

  Query Match             10.8%;  Score 272;  DB 4;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 5e-16;
  Matches   74;  Conservative   28;  Mismatches   78;  Indels   52;  Gaps    9;

Qy          13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRL 72
               || :|| |: ||              |: |||  :|  |:: |||  |: | | |:||  :
Db          11 LLPLLLLLVATT------------GPV-GALTDEEKRLMVELHNLYRAQVSPTASDMLHM 57

Qy          73 DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV---------EV 123
               | : ||  |:| |  |           :|     | | :     |   |
Db          58 RWDEELAAFAKAYARQC----------VW-----GHNKERGRRGENLFAITDEGMDVPLA 102

Qy         124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC----SAGQTAIEAFV 179
               :  |  | : |: :|  |:    | ||||:||| : ::||| | |          :| ||  |
Db         103 MEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLV 162

Qy         180 CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
               | | | ||  | ||   ||::|  || | :        :     |||   :|
Db         163 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-------GYHCKNSLCEPIGSP 203


RESULT 7
US-09-903-603A-285
; Sequence 285, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: GNE.1618P2C12
;  CURRENT APPLICATION NUMBER: US/09/903,603A
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;  CURRENT FILING DATE:  2001-07-11
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-903-603A-285

  Query Match             10.8%;  Score 272;  DB 4;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 5e-16;
  Matches   74;  Conservative   28;  Mismatches   78;  Indels   52;  Gaps    9;

Qy         13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRL 72
              || :|| |: ||              |: |||  :|  |:: |||  |: | | |:||  :
Db         11 LLPLLLLLVATT------------GPV-GALTDEEKRLMVELHNLYRAQVSPTASDMLHM 57

Qy         73 DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV---------EV 123
               | : ||  |:| |  |           :|     | | :   |  |
Db         58 RWDEELAAFAKAYARQC----------VW-----GHNKERGRRGENLFAITDEGMDVPLA 102

Qy        124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC----SAGQTAIEAFV 179
               :  |  | : |: :|  |:     | ||||:||| : ::||| | |       :| ||  |
Db        103 MEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLV 162

Qy        180 CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
              | | | ||  | ||   ||::|  || | :        :     |||   :|
Db        163 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-------GYHCKNSLCEPIGSP 203


RESULT 8
US-09-904-920A-285
; Sequence 285, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,920A
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-920A-285

  Query Match             10.8%;  Score 272;  DB 4;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 5e-16;
  Matches   74;  Conservative   28;  Mismatches   78;  Indels   52;  Gaps    9;

Qy         13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRL 72
              || :|| |: ||              |: |||  :|  |:: |||  |: | | |:||  :
Db         11 LLPLLLLLVATT------------GPV-GALTDEEKRLMVELHNLYRAQVSPTASDMLHM 57
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Qy          73 DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV---------EV 123
               |  :  ||  |:| |  |           :|     | | :    |   |
Db          58 RWDEELAAFAKAYARQC----------VW-----GHNKERGRRGENLFAITDEGMDVPLA 102

Qy         124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC----SAGQTAIEAFV 179
               :  |  | : |: :|  |:    | ||||:||| : ::||| | |       :| ||  |
Db         103 MEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLV 162

Qy         180 CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
               | | | ||  | ||   ||::|  || | :      :     |||   :|
Db         163 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-------GYHCKNSLCEPIGSP 203
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RESULT 9
US-09-909-064-285
; Sequence 285, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-064-285

Query Match 10.8%; Score 272; DB 4; Length 463;
Best Local Similarity 31.9%; Pred. No. 5e-16;
Matches 74; Conservative 28; Mismatches 78; Indels 52; Gaps 9;

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Qy          13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRL 72
               || :|| |: ||             |: |||  :|  |:: |||  |: | | |:||  :
Db          11 LLPLLLLLVATT-----------GPV-GALTDEEKRLMVELHNLYRAQVSPTASDMLHM 57

Qy          73 DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV---------EV 123
               |  :  ||  |:| |  |           :|     | | :    |   |
Db          58 RWDEELAAFAKAYARQC----------VW-----GHNKERGRRGENLFAITDEGMDVPLA 102

Qy         124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC----SAGQTAIEAFV 179
               :  |  | : |: :|  |:    | ||||:||| : ::||| | |       :| ||  |
Db         103 MEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLV 162

Qy         180 CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
               | | | ||  | ||   ||::|  || | :      :     |||   :|
Db         163 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-------GYHCKNSLCEPIGSP 203
```

RESULT 10
US-09-905-381A-285
; Sequence 285, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13

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;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-905-381A-285

  Query Match             10.8%;  Score 272;  DB 4;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 5e-16;
  Matches   74;  Conservative   28;  Mismatches   78;  Indels   52;  Gaps    9;

Qy         13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRL 72
              || :|| |: ||              |: |||  :|  |:: |||  |: | | |:||  :
Db         11 LLPLLLLLVATT-----------GPV-GALTDEEKRLMVELHNLYRAQVSPTASDMLHM 57

Qy         73 DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV---------EV 123
               | : ||  |:| | |           :|     | | :    |   |
Db         58 RWDEELAAFAKAYARQC----------VW-----GHNKERGRRGENLFAITDEGMDVPLA 102

Qy        124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC----SAGQTAIEAFV 179
              :  |  | : |: :|  |:    | ||||:||| : ::||| | |       :| ||  |
Db        103 MEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLV 162

Qy        180 CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
              | | | ||  | ||   ||::|  || | :       :     |||   :|
Db        163 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-------GYHCKNSLCEPIGSP 203


RESULT 11
US-09-906-618-285
; Sequence 285, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,618
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-906-618-285

  Query Match             10.8%;  Score 272;  DB 4;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 5e-16;
  Matches   74;  Conservative   28;  Mismatches   78;  Indels   52;  Gaps    9;

Qy         13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRL 72
              || :|| |: ||              |: |||  :|  |:: |||  |: | | |:||  :
Db         11 LLPLLLLLVATT-----------GPV-GALTDEEKRLMVELHNLYRAQVSPTASDMLHM 57
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Qy          73 DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV---------EV 123
               | : ||  |:| |  |          :|     | | :     |   |
Db          58 RWDEELAAFAKAYARQC----------VW-----GHNKERGRRGENLFAITDEGMDVPLA 102

Qy         124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC----SAGQTAIEAFV 179
               :  |  | : |: :|  |:    | ||||:||| : ::||| | |       :| ||  |
Db         103 MEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLV 162

Qy         180 CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
               | | | ||  | ||   ||::|  || | :        :     |||   :|
Db         163 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-------GYHCKNSLCEPIGSP 203


RESULT 12
US-08-773-368-1
; Sequence 1, Application US/08773368
; Patent No. 5856130
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Goli, Surya K.
;    TITLE OF INVENTION:  NOVEL HUMAN PATHOGENESIS-RELATED
;    TITLE OF INVENTION:  PROTEIN
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/773,368
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy RJ
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0186 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  270 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  1599164
US-08-773-368-1

  Query Match             10.6%;  Score 267;  DB 2;  Length 270;
  Best Local Similarity   31.5%;  Pred. No. 6.8e-16;
  Matches   73;  Conservative   28;  Mismatches   79;  Indels   52;  Gaps    8;

Qy          13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRL 72
               || :|| |: ||             |: |||  :|  |:: |||  |: | | |:||  :
Db          11 LLPLLLLLVATT-----------GPV-GALTDEEKRLMVELHNLYRAQVSPTASDMLHM 57

Qy          73 DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV---------EV 123
               | : ||  |:| |              |  : | | :     |   |
Db          58 RWDEELAAFAKAYA--------------RQXRXGHNKERGRRGENLFAITDEGMDVPLA 102

Qy         124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC----SAGQTAIEAFV 179
               :  |  | : |: :|  |:    | ||||:||| : ::||| | |       :| ||  |
Db         103 MEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLV 162

Qy         180 CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
               | | | ||  | ||   ||::|  || | :        :     |||   :|
Db         163 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-------GYHCKNSLCEPIGSP 203


RESULT 13
US-09-199-887-1
; Sequence 1, Application US/09199887
; Patent No. 6071874
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Goli, Surya K.
;    TITLE OF INVENTION:  NOVEL HUMAN PATHOGENESIS-RELATED
;    TITLE OF INVENTION:  PROTEIN
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/199,887
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/773,368
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy RJ
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0186 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  270 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  1599164
US-09-199-887-1

  Query Match             10.6%;  Score 267;  DB 3;  Length 270;
  Best Local Similarity   31.5%;  Pred. No. 6.8e-16;
  Matches   73;  Conservative   28;  Mismatches   79;  Indels   52;  Gaps    8;

Qy          13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRL 72
               || :|| |: ||             |: |||  :|  |:: |||  |: | | |:||  :
Db          11 LLPLLLLLVATT-----------GPV-GALTDEEKRLMVELHNLYRAQVSPTASDMLHM 57

Qy          73 DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV---------EV 123
               | : ||  |:| |              |  : | | :     |   |
Db          58 RWDEELAAFAKAYA--------------RQXRXGHNKERGRRGENLFAITDEGMDVPLA 102

Qy         124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC----SAGQTAIEAFV 179
               :  |  | : |: :|  |:    | ||||:||| : ::||| | |       :| ||  |
Db         103 MEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLV 162

Qy         180 CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
               | | | ||  | ||   ||::|  || | :        :     |||   :|
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Db        163 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-------GYHCKNSLCEPIGSP 203


RESULT 14
US-09-698-781-3
; Sequence 3, Application US/09698781
; Patent No. 6835822
; GENERAL INFORMATION:
;  APPLICANT:  Rene S. Hubert
;  APPLICANT:  Arthur B. Raitano
;  APPLICANT:  Daniel E.H. Afar
;  APPLICANT:  Steve Chappell Mitchell
;  APPLICANT:  Mary Faris
;  APPLICANT:  Aya Jakobovits
;  TITLE OF INVENTION:  DIAGNOSIS AND THERAPY OF CANCER USING
;  TITLE OF INVENTION:  SGP28-RELATED MOLECULES
;  FILE REFERENCE:  129.23-US-U1
;  CURRENT APPLICATION NUMBER: US/09/698,781
;  CURRENT FILING DATE:  2000-10-27
;  PRIOR APPLICATION NUMBER:  60/162,610
;  PRIOR FILING DATE:  1999-10-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-698-781-3

  Query Match             10.2%;  Score 259;  DB 4;  Length 258;
  Best Local Similarity   27.1%;  Pred. No. 3.4e-15;
  Matches   79;  Conservative   45;  Mismatches  116;  Indels   52;  Gaps   12;

Qy          1 MLHPETSPGRGHLLAVLLALLGTTWAEVWP--PQLQEQAPMAGALNRKESFL---LLSLH 55
              :|||       |  ||| |:    | : |  |  ::: |   ||   :: :   ::: |
Db          4 ILHPALETTAMTLFPVLLFLV----AGLLPSFPANEDKDPAFTALLTTQTQVQREIVNKH 59

Qy         56 NRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGI----PTPSLASGLWRTLQVGWNMQ 111
              | ||  | ||| :| :::|:   |  ||  |  |      |  : |     |: | |:
Db         60 NELRRAVSPPARNMLKMEWNKEAAANAQKWANQCNYRHSNPKDRMTS-----LKCGENLY 114

Qy        112 LLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAG 171
              :  |  :|: : :  || |   :    |    ||  ||||:|| :|  :|||   |
Db        115 MSSAP-SSWSQAIQSWFDEYNDFDFGVGPKTPNAVVGHYTQVVWYSSYLVGCGNAYCPNQ 173

Qy        172 QTAIEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
              :    :|| | | |||    :  :||::|| |: |  :            |||    |
Db        174 KVLKYYYVCQYCPAGNWA--NRLYVPYEQGAPCASCPDNCD---------DGLC---TNG 219

Qy        232 CRMSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREE-ECSCVC 282
              |:           : :|          :: :| | |    |:  : || |
Db        220 CK----------YEDLYSNCK--------SLKLTLTCKHQLVRDSCKASCNC 253


RESULT 15
US-08-773-368-3
; Sequence 3, Application US/08773368
; Patent No. 5856130
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Goli, Surya K.
;    TITLE OF INVENTION:  NOVEL HUMAN PATHOGENESIS-RELATED
;    TITLE OF INVENTION:  PROTEIN
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/773,368
;      FILING DATE:
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy RJ
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0186 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  219 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  847722
US-08-773-368-3

  Query Match             9.2%;  Score 232;  DB 2;  Length 219;
  Best Local Similarity   32.4%;  Pred. No. 7.2e-13;
  Matches   58;  Conservative   28;  Mismatches   61;  Indels   32;  Gaps    7;

Qy         47 ESFL--LLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIP----------T 93
              | |:   : :||: || |:| |:||  :  |  :|||:|:| |: |
Db         21 EDFIKDCVRIHNKFRSEVKPTASDMLYMTWDPALAQIAKAWASNCQFSHNTRLKPPHKLH 80

Qy         94 PSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQL 153
              |:  |       :| |:      : |    :: |: | | |:      | :    | ||||:
Db         81 PNFTS-------LGENIWTGSVPIFSVSSAITNWYDEIQDYNFKTRICKK--VCGHYTQV 131

Qy        154 VWATSSQLGCGRHLCS--AGQTAIE---AFVCAYSPGGNWEVNGKTIIPYKKGAWCSLC 207
              ||| | ::||    |   :|  |:     |:| |.||||:        |||:|| || |
Db        132 VWADSYKVGCAVQFCPKVSGFDALSNGAHFICNYGPGGNYPT-----WPYKRGATCSAC 185


Search completed: February 11, 2005, 19:05:41
Job time : 59 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 11, 2005, 18:56:28 ; Search time 173 Seconds
(without alignments)
1346.798 Million cell updates/sec

Title: US-09-943-664-50
Perfect score: 2529
Sequence: 1 MLHPETSPGRGHLLAVLLAL.....RNRYICQFAQEHISRWGPGS 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2529	100.0	455	2	Q6UXF7	Q6uxf7 homo sapien
2	2438.5	96.4	446	2	Q7Z5K9	Q7z5k9 homo sapien
3	2426.5	95.9	446	2	Q8NCF0	Q8ncf0 homo sapien
4	2423.5	95.8	446	2	Q6DCB3	Q6dcb3 homo sapien
5	1932.5	76.4	473	2	Q7TSP9	Q7tsp9 mus musculu
6	1932.5	76.4	504	2	Q7TSQ0	Q7tsq0 mus musculu
7	1869.5	73.9	477	2	Q7TSQ7	Q7tsq7 mus musculu
8	1869.5	73.9	534	2	Q7TSQ1	Q7tsq1 mus musculu
9	1758	69.5	379	2	Q7TMA7	Q7tma7 mus musculu
10	1611	63.7	301	2	Q8IUW8	Q8iuw8 homo sapien
11	1587	62.8	303	2	Q7Z4U9	Q7z4u9 homo sapien
12	1321	52.2	303	2	Q7Z7I8	Q7z7i8 homo sapien
13	1154	45.6	334	2	Q9BE36	Q9be36 macaca fasc
14	397.5	15.7	156	2	Q96HH2	Q96hh2 homo sapien
15	280	11.1	270	2	Q6ZVG9	Q6zvg9 homo sapien
16	277	11.0	463	2	Q8NBK0	Q8nbk0 homo sapien
17	274.5	10.9	489	2	Q9ET66	Q9et66 mus musculu
18	274.5	10.9	489	2	Q9JJ56	Q9jj56 mus musculu
19	272	10.8	408	2	Q8TCB8	Q8tcb8 homo sapien
20	272	10.8	463	2	Q6UXB8	Q6uxb8 homo sapien
21	260.5	10.3	497	2	Q6UWH0	Q6uwh0 homo sapien
22	259.5	10.3	449	2	Q6P590	Q6p590 homo sapien
23	257.5	10.2	497	2	Q9H0B8	Q9h0b8 homo sapien
24	257	10.2	371	2	Q96K61	Q96k61 homo sapien
25	255	10.1	403	2	Q7SY04	Q7sy04 brachydanio
26	254.5	10.1	255	2	Q9CWG1	Q9cwg1 mus musculu
27	254.5	10.1	258	2	O43692	O43692 homo sapien
28	254.5	10.1	516	2	Q68CY1	Q68cy1 homo sapien
29	254	10.0	523	2	Q98ST5	Q98st5 gallus gall
30	253	10.0	253	2	Q9H3Y0	Q9h3y0 homo sapien
31	252.5	10.0	258	2	Q98ST6	Q98st6 gallus gall
32	252	10.0	245	1	CRS3_HUMAN	P54108 homo sapien
33	252	10.0	258	2	Q99MM7	Q99mm7 mus musculu
34	252	10.0	269	2	Q8BS03	Q8bs03 mus musculu
35	249.5	9.9	428	2	Q8IYL8	Q8iyl8 homo sapien
36	249	9.8	242	2	Q6UWM5	Q6uwm5 homo sapien
37	248.5	9.8	494	2	Q9D2R3	Q9d2r3 mus musculu
38	247.5	9.8	240	1	CRVP_TRIJE	Q7zzn9 trimeresuru
39	246	9.7	495	2	Q8BZQ2	Q8bzq2 mus musculu
40	245	9.7	233	2	Q96L06	Q96l06 homo sapien
41	243	9.6	500	2	Q8CGD2	Q8cgd2 mus musculu
42	241	9.5	233	1	CRVP_TRIST	P60623 trimeresuru
43	240	9.5	188	2	Q9Z0U6	Q9z0u6 rattus norv
44	240	9.5	244	1	CRS2_CAVPO	Q60477 cavia porce
45	239.5	9.5	240	1	CRVP_AGKHA	Q8ji40 agkistrodon
46	236	9.3	1268	1	PGCN_MOUSE	P55066 mus musculu
47	235.5	9.3	500	2	Q9H336	Q9h336 homo sapien
48	235	9.3	239	1	CRVP_OPHHA	Q7zt98 ophiophagus
49	234.5	9.3	240	1	CRVP_CROAT	Q7zt99 crotalus at
50	234.5	9.3	240	1	CRVP_TRIFL	Q8ji39 trimeresuru
51	234	9.3	240	1	CRVP_TRIMU	P79845 trimeresuru
52	234	9.3	507	2	Q99MM6	Q99mm6 mus musculu
53	232	9.2	1268	2	Q6P1E3	Q6p1e3 mus musculu
54	231	9.1	266	1	GLIP_HUMAN	P48060 homo sapien
55	230.5	9.1	238	1	CRV2_NAJAT	Q7zzn8 naja atra (
56	229.5	9.1	280	2	Q7T141	Q7t141 brachydanio
57	228.5	9.0	301	2	Q95QF6	Q95qf6 caenorhabdi
58	228	9.0	245	1	CRS3_HORSE	O19010 equus cabal
59	228	9.0	245	2	Q8HXA1	Q8hxa1 equus cabal
60	227.5	9.0	504	2	Q69HL7	Q69hl7 ciona intes
61	226.5	9.0	1290	2	Q9W6E1	Q9w6e1 gallus gall
62	226	8.9	242	1	HELO_HELHO	Q91055 heloderma h
63	225.5	8.9	300	1	TX31_CONTE	Q7yt83 conus texti
64	225	8.9	236	2	Q9DAG6	Q9dag6 mus musculu
65	225	8.9	240	1	CRVP_AGKPI	Q7zta0 agkistrodon
66	225	8.9	332	2	Q9CQ35	Q9cq35 m mus muscu
67	224	8.9	312	1	YR81_CAEEL	Q09566 caenorhabdi
68	223	8.8	474	2	Q8CHU4	Q8chu4 mus musculu
69	222	8.8	238	1	CRVP_LATSE	Q8ji38 laticauda s
70	221	8.7	239	1	CRV1_NAJAT	Q7t1k6 naja atra (
71	221	8.7	243	1	CRS2_HUMAN	P16562 homo sapien
72	220.5	8.7	244	2	Q8HX97	Q8hx97 equus cabal
73	220	8.7	217	2	O77719	O77719 equus cabal
74	220	8.7	250	2	Q8MHX2	Q8mhx2 equus cabal
75	219	8.7	415	2	O44228	O44228 halocynthia
76	218.5	8.6	287	2	Q8MQ33	Q8mq33 caenorhabdi
77	213.5	8.4	249	1	CRS1_HUMAN	P54107 homo sapien
78	212.5	8.4	237	1	CRVP_RHATT	Q8jgt9 rhabdophis
79	212	8.4	1257	1	PGCN_RAT	P55067 rattus norv
80	209	8.3	244	1	CRS1_MOUSE	Q03401 mus musculu
81	208	8.2	243	2	O88205	O88205 rattus norv
82	207.5	8.2	243	2	Q9R1L4	Q9r1l4 rattus norv
83	207	8.2	244	2	Q91XA3	Q91xa3 mus musculu
84	206.5	8.2	252	2	Q6GN54	Q6gn54 xenopus lae
85	206.5	8.2	287	2	Q75ZI2	Q75zi2 brachydanio
86	205	8.1	238	1	CRV2_LAPHA	Q8uw11 lapemis har
87	205	8.1	1321	1	PGCN_HUMAN	O14594 homo sapien
88	204.5	8.1	162	2	Q6DKY4	Q6dky4 mesocestoid
89	203	8.0	663	2	O44247	O44247 hemicentrot
90	202.5	8.0	247	2	Q6PHC5	Q6phc5 brachydanio
91	201.5	8.0	250	2	Q9D259	Q9d259 mus musculu
92	200.5	7.9	238	1	CRVP_PSEAU	Q8ava4 pseudechis
93	200	7.9	169	2	Q7EYQ2	Q7eyq2 oryza sativ
94	200	7.9	2738	1	PGCV_RAT	Q9erb4 rattus norv
95	200	7.9	3358	1	PGCV_MOUSE	Q62059 mus musculu
96	197.5	7.8	238	1	CRVP_PSEPO	Q8ava3 pseudechis
97	196.5	7.8	392	2	Q9VFY2	Q9vfy2 drosophila
98	196	7.8	2060	2	Q6MZK8	Q6mzk8 homo sapien
99	196	7.8	3396	1	PGCV_HUMAN	P13611 homo sapien
100	195.5	7.7	278	2	Q7Z7B2	Q7z7b2 homo sapien
101	194.5	7.7	238	1	CRV1_LAPHA	Q8uw25 lapemis har
102	194	7.7	1570	2	Q75ZI3	Q75zi3 brachydanio
103	193.5	7.7	243	1	CRS2_MOUSE	P16563 mus musculu
104	191.5	7.6	249	1	CRS1_MACMU	Q9xsd3 macaca mula

105	191	7.6	3562	1	PGCV_CHICK	Q90953	gallus gall
106	190	7.5	3381	1	PGCV_BOVIN	P81282	bos taurus
107	189.5	7.5	1456	1	MANR_MOUSE	Q61830	mus musculu
108	189	7.5	207	2	Q20608	Q20608	caenorhabdi
109	188.5	7.5	246	1	CRS1_RAT	P12020	rattus norv
110	187.5	7.4	205	1	VA5_POLFU	P35780	polistes fu
111	185.5	7.3	161	1	PR1_ARATH	P33154	arabidopsis
112	185.5	7.3	212	2	Q20609	Q20609	caenorhabdi
113	185.5	7.3	1147	2	Q6DIB5	Q6dib5	mus musculu
114	185.5	7.3	1418	2	Q6EEI7	Q6eei7	sus scrofa
115	185	7.3	168	2	Q40397	Q40397	nicotiana g
116	184.5	7.3	567	2	Q8WUL3	Q8wul3	homo sapien
117	184.5	7.3	1140	2	Q96KG7	Q96kg7	homo sapien
118	184.5	7.3	1140	2	Q68DE5	Q68de5	homo sapien
119	184	7.3	158	2	Q6WHB9	Q6whb9	capsicum fr
120	184	7.3	162	2	Q96344	Q96344	brassica na
121	184	7.3	202	1	VA52_VESCR	P35782	vespa crabr
122	183.5	7.3	161	2	Q75QH2	Q75qh2	capsicum ch
123	182.5	7.2	159	1	PR06_LYCES	P04284	lycopersico
124	182	7.2	202	1	VA5_VESMA	P81657	vespa manda
125	181.5	7.2	161	2	Q6IUZ8	Q6iuz8	brassica ca
126	181.5	7.2	176	2	Q8H5R0	Q8h5r0	oryza sativ
127	181.5	7.2	229	2	Q8NA43	Q8na43	homo sapien
128	181.5	7.2	244	2	Q6P303	Q6p303	xenopus tro
129	181.5	7.2	253	2	Q8N6N0	Q8n6n0	homo sapien
130	180.5	7.1	159	1	PR04_LYCES	Q04108	lycopersico
131	180.5	7.1	163	2	O81888	O81888	arabidopsis
132	180.5	7.1	205	1	VA5_POLEX	P35759	polistes ex
133	180.5	7.1	209	1	VA5_POLAN	Q05109	polistes an
134	180	7.1	172	2	Q6YSH3	Q6ysh3	oryza sativ
135	180	7.1	737	2	Q8JZM4	Q8jzm4	mus musculu
136	180	7.1	737	2	Q8R4T6	Q8r4t6	mus musculu
137	179.5	7.1	159	2	Q941G6	Q941g6	solanum tub
138	179.5	7.1	159	2	Q9SC15	Q9sc15	solanum tub
139	179.5	7.1	226	2	Q68KJ9	Q68kj9	polistes ex
140	179	7.1	164	2	Q9XH05	Q9xh05	arabidopsis
141	179	7.1	184	2	Q40597	Q40597	nicotiana t
142	179	7.1	206	1	VA5_POLDO	P81656	polistes do
143	179	7.1	227	2	Q68KJ8	Q68kj8	polistes do
144	178.5	7.1	160	2	Q84YD5	Q84yd5	brassica ju
145	178.5	7.1	1456	1	MANR_HUMAN	P22897	homo sapien
146	178	7.0	202	1	VA51_VESCR	P35781	vespa crabr
147	178	7.0	737	2	Q8NFT8	Q8nft8	homo sapien
148	177.5	7.0	160	2	O24026	O24026	lycopersico
149	177.5	7.0	172	2	Q6YSG3	Q6ysg3	oryza sativ
150	177.5	7.0	241	2	Q801Z0	Q801z0	xenopus lae
151	177.5	7.0	2825	2	O70465	O70465	mus musculu
152	177	7.0	454	2	Q8TB42	Q8tb42	homo sapien
153	176.5	7.0	161	2	Q43392	Q43392	brassica na
154	176.5	7.0	1213	1	JAG3_BRARE	Q90y54	brachydanio
155	176	7.0	176	2	Q6YSH0	Q6ysh0	oryza sativ
156	176	7.0	185	2	Q9SV22	Q9sv22	arabidopsis
157	175.5	6.9	220	2	Q63404	Q63404	rattus norv
158	175	6.9	168	2	O24025	O24025	lycopersico
159	175	6.9	205	2	Q9LZ12	Q9lz12	arabidopsis
160	175	6.9	207	1	VA5_POLSR	Q7z156	polybia scu
161	175	6.9	208	2	Q18543	Q18543	caenorhabdi
162	175	6.9	2771	2	Q9WTS7	Q9wts7	mus musculu
163	174	6.9	168	1	PR1C_TOBAC	P09042	nicotiana t
164	174	6.9	204	1	VA5_VESFL	P35783	vespula fla
165	174	6.9	208	2	Q9N5N4	Q9n5n4	caenorhabdi
166	174	6.9	737	2	Q8VD97	Q8vd97	mus musculu
167	174	6.9	911	1	PGCB_HUMAN	Q96gw7	homo sapien
168	173.5	6.9	212	2	O62508	O62508	caenorhabdi
169	173.5	6.9	213	2	Q93747	Q93747	caenorhabdi
170	173	6.8	206	1	VA5_POLGA	P83377	polistes ga
171	173	6.8	209	2	Q18539	Q18539	caenorhabdi
172	173	6.8	240	2	Q642T6	Q642t6	xenopus tro
173	173	6.8	883	1	PGCB_RAT	P55068	rattus norv
174	172.5	6.8	376	2	Q7F245	Q7f245	oryza sativ
175	172	6.8	163	2	O82086	O82086	zea mays (m
176	172	6.8	164	2	O04000	O04000	oryza sativ
177	172	6.8	164	2	O82714	O82714	triticum ae
178	172	6.8	164	2	Q7F2P0	Q7f2p0	oryza sativ
179	171.5	6.8	192	2	Q7XW56	Q7xw56	oryza sativ
180	171	6.8	168	1	PR1A_TOBAC	P08299	nicotiana t
181	170.5	6.7	159	2	Q8L688	Q81688	solanum phu
182	170.5	6.7	169	2	Q39188	Q39188	arabidopsis
183	170.5	6.7	389	2	Q8R226	Q8r226	mus musculu
184	170	6.7	165	2	Q8LLU7	Q8llu7	oryza sativ
185	170	6.7	165	2	Q6YT69	Q6yt69	oryza sativ
186	170	6.7	170	2	Q6YSG9	Q6ysg9	oryza sativ
187	170	6.7	175	1	PR1A_LYCES	Q08697	lycopersico
188	170	6.7	2415	1	PGCA_HUMAN	P16112	homo sapien
189	169.5	6.7	2590	2	Q9W7R4	Q9w7r4	brachydanio
190	169	6.7	204	1	VA5_VESMC	P35760	vespula mac
191	169	6.7	208	2	Q9N5N3	Q9n5n3	caenorhabdi
192	169	6.7	2352	2	O61240	O61240	halocynthia
193	168.5	6.7	656	1	EFL3_MOUSE	Q80v70	mus musculu
194	168.5	6.7	835	2	Q69ZY6	Q69zy6	mus musculu
195	168.5	6.7	912	1	PGCB_BOVIN	Q28062	bos taurus
196	168.5	6.7	2321	1	NTC3_HUMAN	Q9um47	homo sapien
197	168	6.6	156	2	Q6YT67	Q6yt67	oryza sativ
198	168	6.6	168	2	Q40557	Q40557	nicotiana t
199	168	6.6	204	1	VA5_VESGE	P35784	vespula ger
200	168	6.6	737	2	Q8IYT0	Q8iyt0	homo sapien
201	167.5	6.6	158	2	Q6YSG7	Q6ysg7	oryza sativ
202	167.5	6.6	2346	2	Q9JLC1	Q9jlc1	mus musculu
203	167.5	6.6	2715	2	Q9WTS6	Q9wts6	mus musculu
204	167	6.6	153	2	Q647J6	Q647j6	cynodon dac
205	167	6.6	167	1	PRMS_MAIZE	Q00008	zea mays (m
206	167	6.6	178	2	Q6K4Q3	Q6k4q3	oryza sativ
207	166.5	6.6	159	2	Q8L687	Q8l687	solanum phu
208	166	6.6	207	2	Q9FKL1	Q9fkl1	arabidopsis
209	166	6.6	227	1	VA5_VESVU	Q05110	vespula vul
210	165.5	6.5	799	1	ITBN_DROME	Q27591	drosophila
211	165	6.5	164	2	Q6LBV6	Q6lbv6	nicotiana t
212	165	6.5	168	1	PR1B_TOBAC	P07053	nicotiana t
213	164.5	6.5	167	1	PR1_SAMNI	Q41359	sambucus ni
214	164.5	6.5	173	2	O82715	O82715	triticum ae
215	164.5	6.5	2764	2	Q9WTS5	Q9wts5	mus musculu
216	164	6.5	165	2	O77720	O77720	equus cabal
217	164	6.5	831	2	Q9PU49	Q9pu49	gallus gall
218	164	6.5	2802	2	Q9DER5	Q9der5	gallus gall
219	163.5	6.5	176	2	Q8LMW8	Q8lmw8	oryza sativ
220	163	6.4	164	2	Q94F73	Q94f73	triticum ae
221	163	6.4	164	2	Q43489	Q43489	hordeum vul
222	163	6.4	173	1	PR1_MEDTR	Q40374	medicago tr
223	163	6.4	188	2	Q7XRR1	Q7xrr1	oryza sativ
224	163	6.4	208	2	Q93444	Q93444	caenorhabdi
225	163	6.4	246	2	Q8BMI7	Q8bmi7	mus musculu
226	163	6.4	290	2	O02354	O02354	caenorhabdi
227	163	6.4	292	2	Q8BVU2	Q8bvu2	mus musculu
228	163	6.4	883	1	PGCB_MOUSE	Q61361	mus musculu
229	163	6.4	2531	1	NTC1_RAT	Q07008	rattus norv
230	162.5	6.4	2531	2	O16004	O16004	lytechinus
231	162	6.4	153	2	Q90XE5	Q90xe5	xenopus lae
232	162	6.4	168	2	Q7FP72	Q7fp72	oryza sativ
233	162	6.4	168	2	Q9FE57	Q9fe57	oryza sativ
234	162	6.4	241	1	CRS3_MOUSE	Q03402	mus musculu
235	161.5	6.4	207	2	O16575	O16575	caenorhabdi
236	161.5	6.4	215	1	VA53_DOLMA	P10737	dolichovesp
237	161.5	6.4	2524	1	NOTC_XENLA	P21783	xenopus lae
238	161.5	6.4	2824	2	Q9W7R3	Q9w7r3	brachydanio
239	161	6.4	273	1	CHOD_HUMAN	Q9h9p2	homo sapien
240	161	6.4	273	1	CHOD_MOUSE	Q9cxm0	mus musculu
241	161	6.4	330	2	Q9NT67	Q9nt67	homo sapien
242	161	6.4	674	2	Q8T4N9	Q8t4n9	strongyloce
243	161	6.4	2447	2	O13149	O13149	fugu rubrip
244	160.5	6.3	179	2	Q04106	Q04106	nicotiana t
245	160	6.3	164	1	PR1_HORVU	Q05968	hordeum vul
246	160	6.3	168	2	Q8W3X9	Q8w3x9	solanum tor
247	160	6.3	172	2	Q84J99	Q84j99	oryza sativ
248	160	6.3	186	2	Q9SF44	Q9sf44	arabidopsis
249	160	6.3	206	1	VA5_VESVI	P35787	vespula vid
250	160	6.3	4006	2	O35452	O35452	mus musculu

251	159.5	6.3	162	2	Q9LPM6	Q9lpm6	arabidopsis
252	159.5	6.3	176	2	Q39186	Q39186	arabidopsis
253	159.5	6.3	179	2	O65157	O65157	capsicum an
254	159	6.3	163	2	Q8AXR7	Q8axr7	anguilla ja
255	159	6.3	179	2	Q84J76	Q84j76	oryza sativ
256	159	6.3	209	2	Q18538	Q18538	caenorhabdi
257	159	6.3	594	2	Q9W0A1	Q9w0a1	drosophila
258	159	6.3	594	2	Q9Y151	Q9y151	drosophila
259	159	6.3	1246	1	EFL3_HUMAN	O75095	homo sapien
260	159	6.3	2765	2	Q9R1K2	Q9r1k2	rattus norv
261	158.5	6.3	161	2	Q9ZNS4	Q9zns4	arabidopsis
262	158.5	6.3	728	2	Q90656	Q90656	gallus gall
263	158.5	6.3	1152	2	Q90WM2	Q90wm2	xenopus lae
264	158	6.2	97	2	Q946W2	Q946w2	brassica ca
265	158	6.2	164	1	PR12_HORVU	P35792	hordeum vul
266	158	6.2	424	1	ASP_ANCCA	Q16937	ancylostoma
267	158	6.2	722	1	DLL1_MOUSE	Q61483	mus musculu
268	158	6.2	722	2	Q6PFV7	Q6pfv7	mus musculu
269	157	6.2	168	2	Q6YSF8	Q6ysf8	oryza sativ
270	157	6.2	204	1	VA5_VESPE	P35785	vespula pen
271	157	6.2	207	2	Q93746	Q93746	caenorhabdi
272	157	6.2	211	1	VA3_SOLRI	P35779	solenopsis
273	157	6.2	227	1	VA52_DOLMA	P10736	dolichovesp
274	157	6.2	1308	2	Q9GPM8	Q9gpm8	caenorhabdi
275	157	6.2	2516	2	Q7TQ52	Q7tq52	mus musculu
276	157	6.2	2526	2	Q7TQ51	Q7tq51	mus musculu
277	157	6.2	2531	1	NTC1_MOUSE	Q01705	mus musculu
278	157	6.2	2531	2	Q8K428	Q8k428	mus musculu
279	157	6.2	2531	2	Q7TQ50	Q7tq50	mus musculu
280	156.5	6.2	1574	1	EFL3_RAT	O88281	rattus norv
281	156	6.2	723	1	DLL1_HUMAN	O00548	homo sapien
282	156	6.2	1059	2	Q9VQ47	Q9vq47	drosophila
283	156	6.2	1101	2	Q7KU08	Q7ku08	drosophila
284	156	6.2	2703	1	NOTC_DROME	P07207	drosophila
285	156	6.2	4569	2	Q7PV66	Q7pv66	anopheles g
286	155.5	6.1	301	1	LECI_MOUSE	P24721	mus musculu
287	155.5	6.1	615	2	O57409	O57409	brachydanio
288	155.5	6.1	714	1	DLL1_RAT	P97677	rattus norv
289	155.5	6.1	2622	2	Q7PSV8	Q7psv8	anopheles g
290	155.5	6.1	2653	2	Q25253	Q25253	lucilia cup
291	155	6.1	491	2	Q8TEK2	Q8tek2	homo sapien
292	155	6.1	717	2	P87357	P87357	brachydanio
293	155	6.1	720	2	Q8UWJ4	Q8uwj4	brachydanio
294	155	6.1	883	2	Q80WT7	Q80wt7	mus musculu
295	155	6.1	1441	2	Q867Q2	Q867q2	caenorhabdi
296	154.5	6.1	159	2	Q7XAD8	Q7xad8	oryza sativ
297	154.5	6.1	161	2	Q9LJM5	Q9ljm5	arabidopsis
298	154.5	6.1	172	2	O81889	O81889	arabidopsis
299	154.5	6.1	185	2	Q8LDA3	Q8lda3	arabidopsis
300	154.5	6.1	185	2	Q9FJY1	Q9fjy1	arabidopsis
301	154.5	6.1	721	2	Q91902	Q91902	xenopus lae
302	154.5	6.1	761	2	Q6ST50	Q6st50	mus musculu
303	154.5	6.1	1476	2	Q90285	Q90285	carassius a
304	154.5	6.1	4114	2	O54796	O54796	mus musculu
305	154	6.1	175	2	Q69LU4	Q69lu4	oryza sativ
306	154	6.1	210	2	Q7Z1H1	Q7z1h1	necator ame
307	154	6.1	425	2	O77153	O77153	ancylostoma
308	153.5	6.1	542	2	Q7Q0Z8	Q7q0z8	anopheles g
309	153.5	6.1	678	2	Q68EY0	Q68ey0	xenopus lae
310	153.5	6.1	1315	2	Q71JF2	Q71jf2	mus musculu
311	153.5	6.1	2318	1	NTC3_MOUSE	Q61982	mus musculu
312	153	6.0	164	1	PR13_HORVU	P35793	hordeum vul
313	153	6.0	192	2	Q9UDM2	Q9udm2	homo sapien
314	153	6.0	215	2	Q963I7	Q963i7	heterodera
315	153	6.0	424	2	O76744	O76744	necator ame
316	153	6.0	424	2	Q9XZ41	Q9xz41	ancylostoma
317	153	6.0	772	2	Q6DI48	Q6di48	brachydanio
318	153	6.0	802	2	O57462	O57462	brachydanio
319	152.5	6.0	2528	2	Q8AXP0	Q8axp0	cynops pyrr
320	152	6.0	211	2	Q18549	Q18549	caenorhabdi
321	152	6.0	2109	1	PGCA_CHICK	P07898	gallus gall
322	152	6.0	2109	2	P79787	P79787	gallus gall
323	151.5	6.0	726	2	Q8AW87	Q8aw87	cynops pyrr
324	151.5	6.0	890	2	Q7QJ41	Q7qj41	anopheles g
325	151.5	6.0	1405	2	Q8VHS2	Q8vhs2	mus musculu
326	151.5	6.0	2319	1	NTC3_RAT	Q9r172	rattus norv
327	151.5	6.0	2468	2	Q800E4	Q800e4	brachydanio
328	151	6.0	172	2	Q6YT66	Q6yt66	oryza sativ
329	151	6.0	374	2	Q8TAY8	Q8tay8	homo sapien
330	151	6.0	374	2	Q96NC5	Q96nc5	homo sapien
331	151	6.0	374	2	Q96NF3	Q96nf3	homo sapien
332	151	6.0	374	2	Q9Z209	Q9z209	cricetulus
333	151	6.0	752	2	O42374	O42374	brachydanio
334	151	6.0	1064	1	FBP1_STRPU	P10079	strongyloce
335	151	6.0	1429	1	LI12_CAEEL	P14585	caenorhabdi
336	150.5	6.0	174	2	Q40035	Q40035	hordeum vul
337	150.5	6.0	182	2	Q6YSG4	Q6ysg4	oryza sativ
338	150.5	6.0	280	2	P91429	P91429	caenorhabdi
339	150.5	6.0	1193	2	Q90819	Q90819	gallus gall
340	150.5	6.0	4288	2	Q9NPK9	Q9npk9	homo sapien
341	150.5	6.0	4289	1	TENX_HUMAN	P22105	homo sapien
342	150	5.9	1317	2	Q6IQ50	Q6iq50	homo sapien
343	150	5.9	2471	1	NTC2_HUMAN	Q04721	homo sapien
344	150	5.9	2524	2	Q9GPA5	Q9gpa5	branchiosto
345	149.5	5.9	227	2	Q6FU99	Q6fu99	candida gla
346	149.5	5.9	232	2	Q7Z799	Q7z799	homo sapien
347	149.5	5.9	236	2	Q7Z798	Q7z798	homo sapien
348	149.5	5.9	272	2	Q9R1J9	Q9r1j9	rattus norv
349	149.5	5.9	382	2	Q6UX15	Q6ux15	homo sapien
350	149.5	5.9	870	2	Q8IQG6	Q8iqg6	drosophila
351	149.5	5.9	952	2	Q6ZTA9	Q6zta9	homo sapien
352	149.5	5.9	1214	2	Q90YD2	Q90yd2	xenopus lae
353	149.5	5.9	1270	2	Q9GPN0	Q9gpn0	caenorhabdi
354	149	5.9	167	2	Q8W084	Q8w084	oryza sativ
355	149	5.9	337	2	Q8NHD3	Q8nhd3	homo sapien
356	149	5.9	342	2	Q8NHD5	Q8nhd5	homo sapien
357	149	5.9	569	2	Q8NHD4	Q8nhd4	homo sapien
358	149	5.9	744	2	Q8NHD2	Q8nhd2	homo sapien
359	149	5.9	830	1	SREC_HUMAN	Q14162	homo sapien
360	149	5.9	881	2	Q9W0A0	Q9w0a0	drosophila
361	149	5.9	2192	2	Q804R1	Q804r1	brachydanio
362	149	5.9	2437	1	NTC1_BRARE	P46530	brachydanio
363	148.5	5.9	166	2	Q39187	Q39187	arabidopsis
364	148.5	5.9	969	2	Q96KG6	Q96kg6	homo sapien
365	148.5	5.9	1664	2	Q9TVQ2	Q9tvq2	caenorhabdi
366	148.5	5.9	2428	2	Q8I6X6	Q8i6x6	boophilus m
367	148.5	5.9	2633	2	Q7QK12	Q7qk12	anopheles g
368	148	5.9	161	2	Q9LPM7	Q9lpm7	arabidopsis
369	148	5.9	177	2	Q9SL83	Q9sl83	arabidopsis
370	148	5.9	1455	2	Q86FJ9	Q86fj9	caenorhabdi
371	148	5.9	2365	2	Q6XL67	Q6xl67	bos taurus
372	148	5.9	3523	2	Q7QCP4	Q7qcp4	anopheles g
373	147.5	5.8	236	2	Q7Z7A0	Q7z7a0	homo sapien
374	147.5	5.8	947	2	Q8BKK7	Q8bkk7	mus musculu
375	147.5	5.8	1140	2	Q80T91	Q80t91	mus musculu
376	147.5	5.8	2019	2	Q68FE0	Q68fe0	mus musculu
377	147.5	5.8	2139	1	CRB_DROME	P10040	drosophila
378	147.5	5.8	2364	1	PGCA_BOVIN	P13608	bos taurus
379	147	5.8	156	2	Q84ML7	Q84ml7	triticum ae
380	147	5.8	2470	1	NTC2_MOUSE	O35516	mus musculu
381	146.5	5.8	161	2	Q7XAJ6	Q7xaj6	vitis vinif
382	146.5	5.8	234	1	VA3_SOLIN	P35778	solenopsis
383	146.5	5.8	250	2	Q7YSZ5	Q7ysz5	rhodnius pr
384	146.5	5.8	2146	2	Q9VC97	Q9vc97	drosophila
385	146	5.8	337	2	Q9R1K0	Q9r1k0	rattus norv
386	146	5.8	1218	1	JAG1_HUMAN	P78504	homo sapien
387	146	5.8	2556	1	NTC1_HUMAN	P46531	homo sapien
388	145.5	5.8	205	1	VA5_VESSQ	P35786	vespula squ
389	145.5	5.8	210	2	Q18540	Q18540	caenorhabdi
390	145.5	5.8	241	2	Q6ID87	Q6id87	arabidopsis
391	145.5	5.8	283	2	Q9LNJ2	Q9lnj2	arabidopsis
392	145.5	5.8	382	1	EFL9_MOUSE	Q8k1e3	mus musculu
393	145.5	5.8	620	2	Q9VJU5	Q9vju5	drosophila
394	145.5	5.8	1348	2	Q25199	Q25199	hydra atten
395	145.5	5.8	1479	2	Q64449	Q64449	mus musculu
396	145	5.7	190	2	Q9SW05	Q9sw05	arabidopsis

397	145	5.7	201	2	Q9DDD4	Q9ddd4	gallus gall
398	145	5.7	215	2	Q86F86	Q86f86	schistosoma
399	145	5.7	1415	2	Q8MJ16	Q8mj16	bos taurus
400	144.5	5.7	122	2	Q40448	Q40448	nicotiana g
401	144.5	5.7	415	2	Q75JH0	Q75jh0	dictyosteli
402	144.5	5.7	529	2	Q25058	Q25058	heliocidari
403	144.5	5.7	686	2	Q9DBU9	Q9dbu9	mus musculu
404	144.5	5.7	1687	2	Q61204	Q61204	mus musculu
405	144.5	5.7	1964	1	NTC4_MOUSE	P31695	mus musculu
406	144	5.7	142	2	Q9LLJ4	Q9llj4	pyrus pyrif
407	144	5.7	223	2	Q925G5	Q925g5	mus musculu
408	144	5.7	229	2	Q9QYZ1	Q9qyz1	mus musculu
409	144	5.7	339	2	Q95244	Q95244	sus scrofa
410	144	5.7	465	2	Q7PR44	Q7pr44	anopheles g
411	144	5.7	686	1	DLL4_MOUSE	Q9ji71	mus musculu
412	144	5.7	1176	2	Q6ZWI6	Q6zwi6	homo sapien
413	144	5.7	1212	2	O42347	O42347	gallus gall
414	144	5.7	2333	1	PGCA_CANFA	Q28343	canis famil
415	143.5	5.7	159	2	Q66S03	Q66s03	thalassophr
416	143.5	5.7	301	1	LECI_RAT	P08290	rattus norv
417	143.5	5.7	424	2	Q86GK5	Q86gk5	ancylostoma
418	143.5	5.7	747	2	Q8VHF4	Q8vhf4	mus musculu
419	143.5	5.7	1004	2	Q8CGA7	Q8cga7	mus musculu
420	143.5	5.7	1034	2	Q8VHL7	Q8vhl7	mus musculu
421	143.5	5.7	1034	2	Q8VIK5	Q8vik5	mus musculu
422	143.5	5.7	1202	1	JAG2_RAT	P97607	rattus norv
423	143	5.7	163	2	Q8AXR8	Q8axr8	anguilla ja
424	143	5.7	178	2	Q6K9I7	Q6k9i7	oryza sativ
425	143	5.7	881	1	PRY3_YEAST	P47033	saccharomyc
426	143	5.7	998	2	Q869K4	Q869k4	dictyosteli
427	143	5.7	1216	2	Q90Y55	Q90y55	brachydanio
428	143	5.7	1254	2	Q90Y56	Q90y56	brachydanio
429	143	5.7	1254	2	Q9YHU2	Q9yhu2	brachydanio
430	143	5.7	2471	1	NTC2_RAT	Q9qw30	rattus norv
431	143	5.7	4135	2	O18977	O18977	bos taurus
432	142.5	5.6	180	2	Q6K6I6	Q6k6i6	oryza sativ
433	142.5	5.6	266	2	Q9R1K1	Q9r1k1	rattus norv
434	142.5	5.6	306	1	MMGL_RAT	P49301	rattus norv
435	142	5.6	120	2	Q9LLJ5	Q9llj5	pyrus pyrif
436	142	5.6	134	2	Q9XYX3	Q9xyx3	hydra magni
437	142	5.6	203	1	VA5_DOLAR	Q05108	dolichovesp
438	142	5.6	207	2	Q20603	Q20603	caenorhabdi
439	142	5.6	210	2	Q9SW04	Q9sw04	arabidopsis
440	142	5.6	383	2	O70534	O70534	rattus norv
441	142	5.6	383	2	Q62779	Q62779	rattus norv
442	142	5.6	425	2	Q8I6X0	Q8i6x0	ancylostoma
443	142	5.6	4578	2	O42181	O42181	fugu rubrip
444	141.5	5.6	214	1	ST14_SOLTU	Q41495	solanum tub
445	141.5	5.6	264	2	Q6TS06	Q6ts06	culex quinq
446	141.5	5.6	474	2	Q68EF1	Q68ef1	mus musculu
447	141.5	5.6	1295	1	GLP1_CAEEL	P13508	caenorhabdi
448	141.5	5.6	2037	2	Q7QFS2	Q7qfs2	anopheles g
449	141.5	5.6	2144	2	Q9ULU2	Q9ulu2	homo sapien
450	141	5.6	133	2	Q68DS3	Q68ds3	homo sapien
451	141	5.6	151	2	Q9N0J2	Q9n0j2	bos taurus
452	141	5.6	196	2	O62507	O62507	caenorhabdi
453	141	5.6	202	1	TETN_HUMAN	P05452	homo sapien
454	141	5.6	212	2	Q967G4	Q967g4	heterodera
455	141	5.6	212	2	Q9BID5	Q9bid5	heterodera
456	141	5.6	223	2	Q99P32	Q99p32	mus musculu
457	141	5.6	406	2	Q25059	Q25059	heliocidari
458	141	5.6	559	2	Q9VZ44	Q9vz44	drosophila
459	141	5.6	685	1	DLL4_HUMAN	Q9nr61	homo sapien
460	141	5.6	713	2	Q962W9	Q962w9	podocoryne
461	141	5.6	1218	1	JAG1_MOUSE	Q9qxx0	mus musculu
462	141	5.6	1219	1	JAG1_RAT	Q63722	rattus norv
463	141	5.6	2570	1	SBN1_HUMAN	Q9ny15	homo sapien
464	141	5.6	2656	2	Q9GNU3	Q9gnu3	paracentrot
465	140.5	5.6	174	2	Q9XFB4	Q9xfb4	glycine max
466	140.5	5.6	224	2	Q86FX1	Q86fx1	onchocerca
467	140.5	5.6	241	2	O76663	O76663	caenorhabdi
468	140.5	5.6	664	2	Q9IAT6	Q9iat6	brachydanio
469	140	5.5	223	2	Q99JB4	Q99jb4	m inhibitor
470	140	5.5	1746	1	TENA_PIG	Q29116	sus scrofa
471	140	5.5	2003	1	NTC4_HUMAN	Q99466	homo sapien
472	140	5.5	2705	2	Q9W6V6	Q9w6v6	gallus gall
473	139.5	5.5	140	2	Q8S3W2	Q8s3w2	cucumis sat
474	139.5	5.5	284	2	Q91Y84	Q91y84	mus musculu
475	139.5	5.5	415	2	Q8S9B6	Q8s9b6	volvox cart
476	139.5	5.5	2754	2	Q7PRV4	Q7prv4	anopheles g
477	139	5.5	172	2	Q6K4Q5	Q6k4q5	oryza sativ
478	139	5.5	223	2	Q7TMP8	Q7tmp8	mus musculu
479	139	5.5	227	2	Q7KPY6	Q7kpy6	lucilia cup
480	138.5	5.5	224	2	Q9GPN4	Q9gpn4	onchocerca
481	138.5	5.5	283	1	LECH_MOUSE	P34927	mus musculu
482	138.5	5.5	383	1	EFL9_HUMAN	Q6uy11	homo sapien
483	138	5.5	195	2	Q27340	Q27340	megabalanus
484	138	5.5	204	2	Q20665	Q20665	caenorhabdi
485	138	5.5	204	2	Q6K6I7	Q6k6i7	oryza sativ
486	138	5.5	550	1	KUCR_RAT	P10716	rattus norv
487	138	5.5	794	2	Q8T4P0	Q8t4p0	lytechinus
488	138	5.5	1722	2	Q19350	Q19350	caenorhabdi
489	138	5.5	1961	2	Q6MG89	Q6mg89	rattus norv
490	137.5	5.4	111	2	Q9N0J1	Q9n0j1	bos taurus
491	137.5	5.4	179	1	CD94_PANTR	Q9mz41	pan troglod
492	137.5	5.4	207	1	LECH_CHICK	P02707	gallus gall
493	137.5	5.4	283	1	LECH_RAT	P02706	rattus norv
494	137.5	5.4	306	2	Q7Z4G9	Q7z4g9	homo sapien
495	137.5	5.4	311	1	LECI_HUMAN	P07307	homo sapien
496	137.5	5.4	456	2	Q6CUX7	Q6cux7	kluyveromyc
497	137.5	5.4	589	1	DLL3_RAT	O88671	rattus norv
498	137.5	5.4	1238	1	JAG2_HUMAN	Q9y219	homo sapien
499	137.5	5.4	1242	1	JAG1_BRARE	Q90y57	brachydanio
500	137.5	5.4	1247	1	JAG2_MOUSE	Q9qye5	mus musculu
501	137.5	5.4	2571	1	SBN1_MOUSE	Q8r4y4	mus musculu
502	137	5.4	103	2	Q42126	Q42126	arabidopsis
503	137	5.4	179	2	O54707	O54707	mus musculu
504	137	5.4	179	2	O54708	O54708	mus musculu
505	137	5.4	299	1	PRY1_YEAST	P47032	saccharomyc
506	137	5.4	816	2	O70474	O70474	rattus norv
507	137	5.4	1376	1	CRBH_HUMAN	P82279	homo sapien
508	137	5.4	1406	2	Q8WWY0	Q8wwy0	homo sapien
509	136.5	5.4	179	1	CD94_MACMU	Q9mzk9	macaca mula
510	136.5	5.4	179	2	Q68VD3	Q68vd3	macaca mula
511	136.5	5.4	179	2	Q68VD4	Q68vd4	macaca fasc
512	136.5	5.4	183	2	Q6TRZ7	Q6trz7	culex quinq
513	136.5	5.4	211	2	Q8C351	Q8c351	mus musculu
514	136.5	5.4	570	1	FBP3_STRPU	P49013	strongyloce
515	136.5	5.4	604	2	Q6T3J7	Q6t3j7	drosophila
516	136.5	5.4	742	2	Q8C979	Q8c979	mus musculu
517	136.5	5.4	742	2	Q8K4Q8	Q8k4q8	mus musculu
518	136.5	5.4	833	1	SRC2_MOUSE	P59222	mus musculu
519	136.5	5.4	849	2	Q96SQ3	Q96sq3	homo sapien
520	136.5	5.4	1515	2	Q9DE37	Q9de37	brachydanio
521	136.5	5.4	1607	1	LMG1_MOUSE	P02468	mus musculu
522	136	5.4	147	1	LECE_ANTCR	P06027	anthocidari
523	136	5.4	376	2	Q95LN0	Q951n0	macaca fasc
524	136	5.4	1403	2	Q70E20	Q70e20	mus musculu
525	136	5.4	3191	2	O01335	O01335	caenorhabdi
526	135.5	5.4	211	2	Q6TPK5	Q6tpk5	gallus gall
527	135.5	5.4	399	1	209L_HYLCO	Q8hy10	hylobates c
528	135.5	5.4	450	2	Q8K0H9	Q8k0h9	mus musculu
529	135.5	5.4	459	2	O45132	O45132	haemonchus
530	135.5	5.4	463	2	Q68QF3	Q68qf3	lithobius f
531	135.5	5.4	820	2	Q7Z103	Q7z103	paramecium
532	135.5	5.4	833	1	DL_DROME	P10041	drosophila
533	135.5	5.4	844	2	Q7TSG9	Q7tsg9	mus musculu
534	135.5	5.4	862	1	PGCV_MACNE	Q28858	macaca neme
535	135.5	5.4	1282	2	Q8TER0	Q8ter0	homo sapien
536	135.5	5.4	1458	1	PA2R_RABIT	P49260	oryctolagus
537	135.5	5.4	3004	2	Q24550	Q24550	drosophila
538	135.5	5.4	3004	2	Q9VYN8	Q9vyn8	drosophila
539	135	5.3	134	2	Q9UB05	Q9ub05	hydra atten
540	135	5.3	198	2	Q9XWX3	Q9xwx3	caenorhabdi
541	135	5.3	259	2	Q8T9U5	Q8t9u5	aedes aegyp
542	135	5.3	721	2	Q95YG0	Q95yg0	ciona savig

543	135	5.3	824	2	Q66S04	Q66s04	oikopleura
544	135	5.3	1065	2	Q810H2	Q810h2	mus musculu
545	135	5.3	1115	2	Q7QB67	Q7qb67	anopheles g
546	135	5.3	1529	1	SLT2_HUMAN	O94813	homo sapien
547	135	5.3	2725	2	Q9UKZ4	Q9ukz4	homo sapien
548	135	5.3	2731	2	Q9WTS4	Q9wts4	mus musculu
549	134.5	5.3	417	2	Q8TCR2	Q8tcr2	homo sapien
550	134.5	5.3	422	1	209L_HYLSY	Q8hy11	hylobates s
551	134.5	5.3	598	2	Q6P6N1	Q6p6n1	mus musculu
552	134.5	5.3	742	2	Q8WZA4	Q8wza4	homo sapien
553	134.5	5.3	742	2	Q6P9F2	Q6p9f2	homo sapien
554	134.5	5.3	742	2	Q9BYH7	Q9byh7	homo sapien
555	134.5	5.3	1101	2	Q8IV34	Q8iv34	homo sapien
556	134.5	5.3	1124	1	TIE2_HUMAN	Q02763	homo sapien
557	134.5	5.3	1208	2	Q80YA8	Q80ya8	mus musculu
558	134.5	5.3	1504	1	SLIT_DROME	P24014	drosophila
559	134	5.3	212	2	Q6CSB3	Q6csb3	kluyveromyc
560	134	5.3	338	2	Q7QGY2	Q7qgy2	anopheles g
561	134	5.3	626	2	Q8ND91	Q8nd91	homo sapien
562	134	5.3	775	2	Q8T314	Q8t314	paramecium
563	134	5.3	963	2	Q9GPM9	Q9gpm9	caenorhabdi
564	134	5.3	1479	2	Q9UBG0	Q9ubg0	homo sapien
565	134	5.3	1479	2	Q9Y5P9	Q9y5p9	homo sapien
566	134	5.3	1484	2	Q7LGE7	Q7lge7	homo sapien
567	134	5.3	1523	1	SLT3_RAT	O88280	rattus norv
568	134	5.3	1551	2	Q9NGV4	Q9ngv4	drosophila
569	134	5.3	3222	2	Q6V0I7	Q6v0i7	homo sapien
570	134	5.3	3396	2	Q9VM55	Q9vm55	drosophila
571	133.5	5.3	158	2	Q90WI7	Q90wi7	bungarus fa
572	133.5	5.3	179	1	CD94_PONPY	Q8mhy9	pongo pygma
573	133.5	5.3	256	1	209P_MACMU	Q8mis5	macaca mula
574	133.5	5.3	328	1	SCGF_MOUSE	O88200	mus musculu
575	133.5	5.3	778	2	Q9IBG4	Q9ibg4	xenopus lae
576	133.5	5.3	1532	2	Q90994	Q90994	gallus gall
577	133.5	5.3	1714	2	Q90995	Q90995	gallus gall
578	133.5	5.3	1808	1	TENA_CHICK	P10039	gallus gall
579	133	5.3	134	2	Q9XYX2	Q9xyx2	hydra atten
580	133	5.3	374	1	WIF1_XENLA	Q9w6f8	xenopus lae
581	133	5.3	738	2	Q90Z45	Q90z45	gallus gall
582	133	5.3	802	2	Q6DF97	Q6df97	xenopus lae
583	133	5.3	1521	1	SLT2_MOUSE	Q9r1b9	mus musculu
584	133	5.3	1581	2	O73809	O73809	fugu rubrip
585	132.5	5.2	179	1	CD94_HUMAN	Q13241	homo sapien
586	132.5	5.2	217	2	Q7Z1H0	Q7z1h0	ancylostoma
587	132.5	5.2	742	2	Q8VIF6	Q8vif6	mus musculu
588	132.5	5.2	798	2	Q75WV8	Q75wv8	branchiosto
589	132.5	5.2	1072	2	Q80YS4	Q80ys4	mus musculu
590	132	5.2	168	2	Q8WPD0	Q8wpd0	asterina pe
591	132	5.2	173	1	LEC2_MEGRO	P17346	megabalanus
592	132	5.2	258	2	Q6FSU9	Q6fsu9	candida gla
593	132	5.2	585	2	Q9U0E2	Q9u0e2	tribolium c
594	132	5.2	642	2	P79941	P79941	xenopus lae
595	132	5.2	647	2	Q6P3V5	Q6p3v5	homo sapien
596	132	5.2	808	2	Q9XXU1	Q9xxu1	caenorhabdi
597	132	5.2	810	2	Q9NL29	Q9nl29	caenorhabdi
598	132	5.2	887	2	Q9U1T9	Q9u1t9	caenorhabdi
599	131.5	5.2	173	1	LIT2_MOUSE	Q08731	mus musculu
600	131.5	5.2	280	2	Q7ZXT0	Q7zxt0	xenopus lae
601	131.5	5.2	308	2	Q17450	Q17450	caenorhabdi
602	131.5	5.2	796	2	Q8MY77	Q8my77	branchiosto
603	131.5	5.2	832	2	Q80YX0	Q80yx0	mus musculu
604	131.5	5.2	1083	2	Q9QW24	Q9qw24	rattus sp.
605	131.5	5.2	2019	2	Q64706	Q64706	mus musculu
606	131.5	5.2	2019	2	Q80YX2	Q80yx2	mus musculu
607	131.5	5.2	2110	2	Q80YX1	Q80yx1	mus musculu
608	131.5	5.2	4599	1	LR1B_MOUSE	Q9ji18	mus musculu
609	131	5.2	87	2	Q70Y31	Q70y31	physcomitre
610	131	5.2	218	2	O77221	O77221	ancylostoma
611	131	5.2	245	2	Q6BK29	Q6bk29	debaryomyce
612	131	5.2	383	1	DLK_HUMAN	P80370	homo sapien
613	131	5.2	383	2	Q969Y6	Q969y6	homo sapien
614	131	5.2	798	1	ITB7_HUMAN	P26010	homo sapien
615	131	5.2	845	2	Q6AVG4	Q6avg4	oryza sativ
616	131	5.2	1523	1	SLT3_HUMAN	O75094	homo sapien
617	131	5.2	1523	1	SLT3_MOUSE	Q9wvb4	mus musculu
618	131	5.2	1799	1	LMB2_MOUSE	Q61292	mus musculu
619	131	5.2	2811	2	Q7Q434	Q7q434	anopheles g
620	131	5.2	3567	2	Q9ES77	Q9es77	mus musculu
621	130.5	5.2	399	1	209L_HYLLA	Q8hy12	hylobates l
622	130.5	5.2	812	2	Q6T683	Q6t683	gallus gall
623	130.5	5.2	1122	1	TIE2_MOUSE	Q02858	mus musculu
624	130.5	5.2	2201	1	TENA_HUMAN	P24821	homo sapien
625	130	5.1	223	1	NK12_MOUSE	P27812	mus musculu
626	130	5.1	260	2	Q7TSU6	Q7tsu6	mus musculu
627	130	5.1	277	2	Q80ZY1	Q80zy1	mus musculu
628	130	5.1	316	2	Q8IUN9	Q8iun9	homo sapien
629	130	5.1	507	2	Q8MS81	Q8ms81	drosophila
630	130	5.1	642	2	Q7ZXT4	Q7zxt4	xenopus lae
631	130	5.1	1045	2	Q8T3A6	Q8t3a6	caenorhabdi
632	130	5.1	1070	2	Q8T3A7	Q8t3a7	caenorhabdi
633	130	5.1	1111	2	Q9XWD6	Q9xwd6	caenorhabdi
634	129.5	5.1	159	2	Q7T1Q3	Q7t1q3	echidna del
635	129.5	5.1	308	2	Q17452	Q17452	caenorhabdi
636	129.5	5.1	316	2	Q6C9V2	Q6c9v2	yarrowia li
637	129.5	5.1	328	1	SCGF_RAT	O88201	rattus norv
638	129.5	5.1	379	2	Q6UXI1	Q6uxi1	homo sapien
639	129.5	5.1	385	1	DLK_MOUSE	Q09163	mus musculu
640	129.5	5.1	385	2	Q925U3	Q925u3	mus musculu
641	129.5	5.1	448	2	Q8MXZ4	Q8mxz4	dictyosteli
642	129.5	5.1	515	1	APX1_CAEEL	P41990	caenorhabdi
643	129.5	5.1	806	1	ITB7_MOUSE	P26011	mus musculu
644	129.5	5.1	1162	2	Q8WTP0	Q8wtp0	halocynthia
645	129.5	5.1	1275	2	Q99PW0	Q99pw0	rattus norv
646	129.5	5.1	1427	2	Q8VIB7	Q8vib7	mesocricetu
647	129.5	5.1	1432	2	Q99J86	Q99j86	rattus norv
648	129.5	5.1	1810	2	Q90824	Q90824	gallus gall
649	129.5	5.1	2515	2	Q24551	Q24551	drosophila
650	129.5	5.1	2731	2	O18366	O18366	drosophila
651	129.5	5.1	2731	2	O61307	O61307	drosophila
652	129.5	5.1	2731	2	Q9VNU6	Q9vnu6	drosophila
653	129	5.1	160	2	Q7SZ75	Q7sz75	xenopus lae
654	129	5.1	190	2	Q7XW57	Q7xw57	oryza sativ
655	129	5.1	246	2	Q9N3I3	Q9n3i3	caenorhabdi
656	129	5.1	592	2	Q7QT99	Q7qt99	giardia lam
657	129	5.1	650	2	Q7Q0M5	Q7q0m5	anopheles g
658	129	5.1	762	2	O42373	O42373	brachydanio
659	129	5.1	801	2	P91774	P91774	pacifastacu
660	129	5.1	1136	1	TIE1_BOVIN	Q06805	bos taurus
661	129	5.1	1203	2	Q86KZ0	Q86kz0	dictyosteli
662	129	5.1	2906	2	Q9WUH9	Q9wuh9	rattus norv
663	129	5.1	2972	2	P90891	P90891	caenorhabdi
664	128.5	5.1	155	1	PLC_HALLA	P82596	haliotis la
665	128.5	5.1	191	2	Q9ZNX5	Q9znx5	camellia si
666	128.5	5.1	196	2	Q9EPW4	Q9epw4	mus musculu
667	128.5	5.1	208	1	209E_MOUSE	Q91zw7	mus musculu
668	128.5	5.1	290	2	Q9DAU5	Q9dau5	mus musculu
669	128.5	5.1	299	2	Q8BX64	Q8bx64	mus musculu
670	128.5	5.1	379	1	WIF1_HUMAN	Q9y5w5	homo sapien
671	128.5	5.1	420	2	Q8I499	Q8i499	cupiennius
672	128.5	5.1	450	2	Q869J7	Q869j7	glomeris ma
673	128.5	5.1	1316	2	Q96JU7	Q96ju7	homo sapien
674	128.5	5.1	1534	1	SLT1_HUMAN	O75093	homo sapien
675	128.5	5.1	1609	1	LMG1_HUMAN	P11047	homo sapien
676	128.5	5.1	3075	1	LMA1_HUMAN	P25391	homo sapien
677	128	5.1	117	2	Q8WS91	Q8ws91	heterodera
678	128	5.1	165	2	Q9SL82	Q9sl82	arabidopsis
679	128	5.1	220	2	O44931	O44931	onchocerca
680	128	5.1	268	2	Q7Z6N1	Q7z6n1	homo sapien
681	128	5.1	271	2	Q9BWP8	Q9bwp8	homo sapien
682	128	5.1	276	2	Q6BTJ8	Q6btj8	debaryomyce
683	128	5.1	473	1	FP2_MYTGA	Q25464	mytilus gal
684	128	5.1	587	2	Q8NBS4	Q8nbs4	homo sapien
685	128	5.1	736	2	Q7QTA2	Q7qta2	giardia lam
686	128	5.1	767	2	Q66PY4	Q66py4	manduca sex
687	128	5.1	1028	2	O60283	O60283	homo sapien
688	128	5.1	1233	2	Q6ZSN4	Q6zsn4	homo sapien

689	128	5.1	1379	2	Q6T256	Q6t256	homo sapien
690	128	5.1	1530	2	Q90WZ3	Q90wz3	xenopus lae
691	127.5	5.0	197	1	CLE1_HUMAN	O75596	homo sapien
692	127.5	5.0	202	1	TETN_MOUSE	P43025	mus musculu
693	127.5	5.0	202	2	Q8CFZ6	Q8cfz6	mus musculu
694	127.5	5.0	206	2	Q6UXF5	Q6uxf5	homo sapien
695	127.5	5.0	217	2	Q7Z1H2	Q7z1h2	ancylostoma
696	127.5	5.0	220	2	O44932	O44932	brugia mala
697	127.5	5.0	308	2	Q7QDM9	Q7qdm9	anopheles g
698	127.5	5.0	331	2	Q6AZ45	Q6az45	rattus norv
699	127.5	5.0	378	2	Q9N1X4	Q9n1x4	sus scrofa
700	127.5	5.0	1429	1	ATRN_HUMAN	O75882	homo sapien
701	127	5.0	154	2	Q8T9U0	Q8t9u0	aedes aegyp
702	127	5.0	221	2	O18347	O18347	dirofilaria
703	127	5.0	403	2	O18375	O18375	drosophila
704	127	5.0	404	1	C209_PONPY	Q8hy00	pongo pygma
705	127	5.0	618	1	DLL3_HUMAN	Q9nyj7	homo sapien
706	127	5.0	674	2	Q7YZH9	Q7yzh9	monosiga br
707	127	5.0	1007	2	Q90ZN3	Q90zn3	gallus gall
708	126.5	5.0	158	1	LECG_TRIST	Q9ygp1	trimeresuru
709	126.5	5.0	161	2	Q9M0C8	Q9m0c8	arabidopsis
710	126.5	5.0	220	2	O97149	O97149	wuchereria
711	126.5	5.0	309	2	Q8VH32	Q8vh32	mus musculu
712	126.5	5.0	309	2	Q8VH33	Q8vh33	mus musculu
713	126.5	5.0	311	2	Q6CA40	Q6ca40	yarrowia li
714	126.5	5.0	331	1	FCE2_MOUSE	P20693	mus musculu
715	126.5	5.0	333	2	O17510	O17510	botryllus s
716	126.5	5.0	493	2	Q7ZTJ2	Q7ztj2	xenopus lae
717	126.5	5.0	1408	1	SERR_DROME	P18168	drosophila
718	126.5	5.0	1501	2	Q75JA5	Q75ja5	dictyosteli
719	126.5	5.0	4391	1	PGBM_HUMAN	P98160	homo sapien
720	126	5.0	219	2	Q9ULY5	Q9uly5	homo sapien
721	126	5.0	238	2	Q8QGG9	Q8qgg9	gallus gall
722	126	5.0	272	2	Q9DC75	Q9dc75	mus musculu
723	126	5.0	689	2	Q80ZL5	Q80zl5	mus musculu
724	126	5.0	1021	2	Q6NUU4	Q6nuu4	brachydanio
725	126	5.0	1407	2	Q9VB65	Q9vb65	drosophila
726	126	5.0	1487	2	Q62028	Q62028	mus musculu
727	126	5.0	1593	2	Q8JHV8	Q8jhv8	brachydanio
728	126	5.0	3623	2	O70244	O70244	rattus norv
729	125.5	5.0	376	1	209L_GORGO	Q8hy06	gorilla gor
730	125.5	5.0	425	2	Q9NAK5	Q9nak5	caenorhabdi
731	125.5	5.0	872	2	Q6ZNB8	Q6znb8	homo sapien
732	125.5	5.0	3333	1	LMA3_MOUSE	Q61789	mus musculu
733	125.5	5.0	4599	1	LR1B_HUMAN	Q9nzr2	homo sapien
734	125.5	5.0	4699	2	Q9V383	Q9v383	drosophila
735	125	4.9	126	2	Q7T228	Q7t228	bothrops ja
736	125	4.9	135	1	LECG_CROAT	P21963	crotalus at
737	125	4.9	180	2	Q868C2	Q868c2	mytilus tro
738	125	4.9	180	2	Q86M01	Q86m01	mytilus tro
739	125	4.9	320	2	Q8N780	Q8n780	homo sapien
740	125	4.9	572	2	Q7QR15	Q7qr15	giardia lam
741	125	4.9	792	2	Q90Z43	Q90z43	gallus gall
742	125	4.9	950	2	Q90Z44	Q90z44	gallus gall
743	125	4.9	1095	2	Q90XG4	Q90xg4	gallus gall
744	125	4.9	1125	1	TIE2_BOVIN	Q06807	bos taurus
745	125	4.9	1463	1	PA2R_BOVIN	P49259	bos taurus
746	125	4.9	1722	1	LY75_HUMAN	O60449	homo sapien
747	125	4.9	1722	1	LY75_MESAU	Q920p9	mesocricetu
748	125	4.9	1817	2	Q7Z575	Q7z575	homo sapien
749	125	4.9	1827	2	Q8JHV6	Q8jhv6	brachydanio
750	125	4.9	1873	2	Q7Z577	Q7z577	homo sapien
751	125	4.9	2911	1	FBN2_HUMAN	P35556	homo sapien
752	124.5	4.9	158	2	Q9R0V8	Q9r0v8	rattus norv
753	124.5	4.9	266	2	Q7R369	Q7r369	giardia lam
754	124.5	4.9	295	2	Q9VIX0	Q9vix0	drosophila
755	124.5	4.9	309	2	Q63097	Q63097	rattus norv
756	124.5	4.9	331	2	Q8R4T3	Q8r4t3	rattus norv
757	124.5	4.9	374	1	PSPD_RAT	P35248	rattus norv
758	124.5	4.9	435	2	O45484	O45484	caenorhabdi
759	124.5	4.9	475	2	Q6KAQ6	Q6kaq6	mus musculu
760	124.5	4.9	487	2	Q8MSX5	Q8msx5	drosophila
761	124.5	4.9	1138	1	TIE1_HUMAN	P35590	homo sapien
762	124.5	4.9	1410	2	Q20204	Q20204	caenorhabdi
763	124.5	4.9	1441	2	Q7Z3G3	Q7z3g3	homo sapien
764	124.5	4.9	1497	2	Q8NBT9	Q8nbt9	homo sapien
765	124.5	4.9	1704	2	Q94446	Q94446	chironomus
766	124.5	4.9	4544	1	LRP1_HUMAN	Q07954	homo sapien
767	124	4.9	177	1	PRB1_TOBAC	P11670	nicotiana t
768	124	4.9	360	2	Q7Q1I4	Q7q114	anopheles g
769	124	4.9	368	2	Q6CSB2	Q6csb2	kluyveromyc
770	124	4.9	884	2	Q7QT01	Q7qt01	giardia lam
771	124	4.9	1353	2	Q00546	Q00546	gallus gall
772	124	4.9	1372	2	P91526	P91526	caenorhabdi
773	124	4.9	1529	2	Q7ZXI2	Q7zxi2	xenopus lae
774	124	4.9	1823	2	Q7PRP5	Q7prp5	anopheles g
775	123.5	4.9	163	2	Q9IB90	Q9ib90	cyprinus ca
776	123.5	4.9	182	2	Q7XRQ8	Q7xrq8	oryza sativ
777	123.5	4.9	223	2	Q925G3	Q925g3	m natural k
778	123.5	4.9	585	2	Q80W06	Q80w06	mus musculu
779	123.5	4.9	592	1	DLL3_MOUSE	O88516	mus musculu
780	123.5	4.9	647	2	Q6PAP2	Q6pap2	mus musculu
781	123.5	4.9	1134	1	TIE1_MOUSE	Q06806	mus musculu
782	123.5	4.9	1134	2	Q8BGI2	Q8bgi2	m mus muscu
783	123.5	4.9	1323	2	Q7Z387	Q7z387	homo sapien
784	123.5	4.9	5703	1	MU5B_HUMAN	Q9hc84	homo sapien
785	123	4.9	135	1	LECG_LACST	Q9psm4	lachesis st
786	123	4.9	166	1	LITA_HUMAN	P05451	homo sapien
787	123	4.9	188	2	Q9W0I2	Q9w0i2	drosophila
788	123	4.9	236	2	Q8UUM9	Q8uum9	oryzias lat
789	123	4.9	376	2	Q8IRH8	Q8irh8	drosophila
790	123	4.9	421	2	Q9NKE1	Q9nke1	drosophila
791	123	4.9	673	2	Q86WK8	Q86wk8	homo sapien
792	123	4.9	955	2	Q96DN2	Q96dn2	homo sapien
793	123	4.9	2330	1	EFL4_MOUSE	P60882	mus musculu
794	123	4.9	2729	2	Q6PQK6	Q6pqk6	paramecium
795	123	4.9	3084	1	LMA1_MOUSE	P19137	mus musculu
796	122.5	4.8	166	1	TETN_CARSP	P26258	carcharhinu
797	122.5	4.8	178	2	Q7Q7F8	Q7q7f8	anopheles g
798	122.5	4.8	205	2	Q75FA9	Q75fa9	ashbya goss
799	122.5	4.8	276	2	Q6MV86	Q6mv86	neurospora
800	122.5	4.8	293	1	EFL8_MOUSE	Q6guq1	mus musculu
801	122.5	4.8	304	1	MMGL_MOUSE	P49300	mus musculu
802	122.5	4.8	304	2	Q91YT3	Q91yt3	mus musculu
803	122.5	4.8	332	2	Q7SG93	Q7sg93	neurospora
804	122.5	4.8	353	2	Q69F40	Q69f40	homo sapien
805	122.5	4.8	356	2	Q96FY1	Q96fy1	homo sapien
806	122.5	4.8	374	2	Q6IRS7	Q6irs7	rattus norv
807	122.5	4.8	427	1	C209_GORGO	Q8hxz8	gorilla gor
808	122.5	4.8	669	2	Q6DFA5	Q6dfa5	xenopus lae
809	122.5	4.8	1531	1	SLT1_MOUSE	Q80tr4	mus musculu
810	122.5	4.8	2923	1	CLR2_HUMAN	Q9hcu4	homo sapien
811	122.5	4.8	3277	2	Q6VU67	Q6vu67	homo sapien
812	122.5	4.8	3333	2	Q6VU68	Q6vu68	homo sapien
813	122.5	4.8	3333	2	Q76E14	Q76e14	homo sapien
814	122.5	4.8	23015	2	Q8IQ18	Q8iq18	drosophila
815	122	4.8	164	2	Q6TRS6	Q6trs6	bothrops ja
816	122	4.8	374	1	PSPD_MOUSE	P50404	mus musculu
817	122	4.8	438	2	Q8I497	Q8i497	cupiennius
818	122	4.8	451	2	Q86GK4	Q86gk4	ancylostoma
819	122	4.8	508	2	Q86GK6	Q86gk6	ancylostoma
820	122	4.8	866	1	SRC2_HUMAN	Q96gp6	homo sapien
821	122	4.8	1358	2	Q15568	Q15568	homo sapien
822	122	4.8	1358	2	Q92752	Q92752	homo sapien
823	122	4.8	1501	2	Q75JS9	Q75js9	dictyosteli
824	122	4.8	1723	1	LY75_MOUSE	Q60767	mus musculu
825	122	4.8	2871	1	FBN1_BOVIN	P98133	bos taurus
826	122	4.8	3102	2	O45614	O45614	caenorhabdi
827	121.5	4.8	122	2	Q6XHL8	Q6xhl8	drosophila
828	121.5	4.8	158	2	Q90WI8	Q90wi8	bungarus fa
829	121.5	4.8	195	2	Q75N89	Q75n89	homo sapien
830	121.5	4.8	269	2	Q8NC23	Q8nc23	homo sapien
831	121.5	4.8	292	2	Q14538	Q14538	homo sapien
832	121.5	4.8	308	2	O46370	O46370	bos taurus
833	121.5	4.8	358	1	C209_PAPHA	Q8hy04	papio hamad
834	121.5	4.8	381	1	C209_CERAE	P60883	cercopithec

835	121.5	4.8	381	1	C209_HYLSY	Q8hy02	hylobates s
836	121.5	4.8	404	1	C209_HYLCO	Q8hy01	hylobates c
837	121.5	4.8	450	1	C209_HYLLA	Q8hy03	hylobates l
838	121.5	4.8	580	2	Q8HZ48	Q8hz48	oryctolagus
839	121.5	4.8	837	2	Q86G85	Q86g85	pseudoplusi
840	121.5	4.8	1356	2	Q05546	Q05546	rattus norv
841	121.5	4.8	1358	2	Q8BYI9	Q8byi9	mus musculu
842	121.5	4.8	1365	2	Q75N88	Q75n88	homo sapien
843	121.5	4.8	1639	1	LMG1_DROME	P15215	drosophila
844	121.5	4.8	2014	2	Q22774	Q22774	caenorhabdi
845	121.5	4.8	2871	1	FBN1_HUMAN	P35555	homo sapien
846	121.5	4.8	2871	1	FBN1_MOUSE	Q61554	mus musculu
847	121.5	4.8	2871	1	FBN1_PIG	Q9tv36	sus scrofa
848	121.5	4.8	2871	2	Q75N87	Q75n87	homo sapien
849	121.5	4.8	3623	2	O60494	O60494	homo sapien
850	121	4.8	166	1	LITB_HUMAN	P48304	homo sapien
851	121	4.8	196	2	Q95XZ4	Q95xz4	caenorhabdi
852	121	4.8	217	2	Q64228	Q64228	mus sp. nk1
853	121	4.8	220	1	NK14_MOUSE	P27814	mus musculu
854	121	4.8	381	1	C209_MACNE	Q95lc6	macaca neme
855	121	4.8	404	1	C209_HUMAN	Q9nnx6	homo sapien
856	121	4.8	404	1	C209_MACMU	Q95j96	macaca mula
857	121	4.8	800	2	Q8SQB9	Q8sqb9	bos taurus
858	121	4.8	1512	2	Q9DE36	Q9de36	brachydanio
859	121	4.8	1723	2	Q6WY07	Q6wy07	bos taurus
860	121	4.8	2531	2	Q8MPZ2	Q8mpz2	caenorhabdi
861	121	4.8	2560	2	Q21980	Q21980	caenorhabdi
862	121	4.8	3014	1	CLR1_HUMAN	Q9nyq6	homo sapien
863	120.5	4.8	155	2	Q7YSR5	Q7ysr5	drosophila
864	120.5	4.8	155	2	Q7Z1J0	Q7z1j0	drosophila
865	120.5	4.8	155	2	Q7Z1J1	Q7z1j1	drosophila
866	120.5	4.8	201	2	Q9NA92	Q9na92	caenorhabdi
867	120.5	4.8	360	2	Q75FB0	Q75fb0	ashbya goss
868	120.5	4.8	399	1	209L_HUMAN	Q9h2x3	homo sapien
869	120.5	4.8	445	1	209L_PANTR	Q8hyc0	pan troglod
870	120.5	4.8	520	2	Q18424	Q18424	caenorhabdi
871	120.5	4.8	668	2	Q6PAE0	Q6pae0	xenopus lae
872	120.5	4.8	715	2	Q6DCW5	Q6dcw5	xenopus lae
873	120.5	4.8	787	2	Q80VI3	Q80vi3	mus musculu
874	120.5	4.8	788	2	Q8IXB8	Q8ixb8	homo sapien
875	120.5	4.8	950	2	Q8MQN5	Q8mqn5	drosophila
876	120.5	4.8	1095	2	Q60784	Q60784	mus musculu
877	120.5	4.8	1378	2	Q68HV2	Q68hv2	mus musculu
878	120.5	4.8	1444	2	Q6A051	Q6a051	mus musculu
879	120.5	4.8	2192	2	O01768	O01768	caenorhabdi
880	120.5	4.8	2872	2	Q9WUH8	Q9wuh8	rattus norv
881	120.5	4.8	2907	1	FBN2_MOUSE	Q61555	mus musculu
882	120.5	4.8	3857	2	O88840	O88840	mus musculu
883	120.5	4.8	4545	2	Q91ZX7	Q91zx7	mus musculu
884	120.5	4.8	4545	2	Q920Y4	Q920y4	mus musculu
885	120	4.7	158	2	Q6QX33	Q6qx33	bothrops in
886	120	4.7	180	2	Q86M03	Q86m03	mytilus gal
887	120	4.7	277	2	Q8WYH1	Q8wyh1	homo sapien
888	120	4.7	500	2	Q864U4	Q864u4	bos taurus
889	120	4.7	640	2	O09182	O09182	rattus norv
890	120	4.7	867	2	Q68YS7	Q68ys7	olive floun
891	120	4.7	1294	1	TENN_HUMAN	Q9uqp3	homo sapien
892	120	4.7	1918	2	Q86AS3	Q86as3	dictyosteli
893	120	4.7	2124	1	PGCA_RAT	P07897	rattus norv
894	120	4.7	2559	1	SBN2_MOUSE	Q8r4u0	mus musculu
895	120	4.7	2596	2	Q6W3C6	Q6w3c6	caenorhabdi
896	120	4.7	4589	2	Q9WU10	Q9wu10	rattus norv
897	119.5	4.7	159	2	Q7T1Q4	Q7t1q4	gymnothorax
898	119.5	4.7	163	2	Q8AWH4	Q8awh4	carassius a
899	119.5	4.7	271	2	Q7T0T0	Q7t0t0	xenopus lae
900	119.5	4.7	274	2	Q7Q9A6	Q7q9a6	anopheles g
901	119.5	4.7	427	1	C209_PANTR	Q8hxz7	pan troglod
902	119.5	4.7	675	1	YMV2_CAEEL	P34504	caenorhabdi
903	119.5	4.7	967	2	Q6BEV9	Q6bev9	caenorhabdi
904	119.5	4.7	1228	2	Q76P25	Q76p25	dictyosteli
905	119.5	4.7	1502	2	Q9UPZ6	Q9upz6	homo sapien
906	119.5	4.7	1584	1	BAI1_HUMAN	O14514	homo sapien
907	119.5	4.7	4545	2	Q61291	Q61291	mus musculu
908	119	4.7	139	2	Q8W377	Q8w377	oryza sativ
909	119	4.7	139	2	Q7XD87	Q7xd87	oryza sativ
910	119	4.7	153	2	Q7Q7F9	Q7q7f9	anopheles g
911	119	4.7	180	2	Q86M05	Q86m05	mytilus gal
912	119	4.7	180	2	Q86M06	Q86m06	mytilus gal
913	119	4.7	187	2	Q6VNB6	Q6vnb6	strongyloce
914	119	4.7	231	2	Q8IFT6	Q8ift6	ostertagia
915	119	4.7	270	2	Q7Q8U6	Q7q8u6	anopheles g
916	119	4.7	357	2	Q7QER8	Q7qer8	anopheles g
917	119	4.7	574	2	Q7R5J3	Q7r5j3	giardia lam
918	119	4.7	616	2	Q20852	Q20852	caenorhabdi
919	119	4.7	647	2	Q8MLX3	Q8mlx3	caenorhabdi
920	119	4.7	647	2	Q8MM25	Q8mm25	caenorhabdi
921	119	4.7	647	2	Q8MV49	Q8mv49	caenorhabdi
922	119	4.7	647	2	Q8MV50	Q8mv50	caenorhabdi
923	119	4.7	647	2	Q8MV51	Q8mv51	caenorhabdi
924	119	4.7	647	2	Q8MV52	Q8mv52	caenorhabdi
925	119	4.7	647	2	Q8MV53	Q8mv53	caenorhabdi
926	119	4.7	647	2	Q8MV54	Q8mv54	caenorhabdi
927	119	4.7	661	2	Q9TVY6	Q9tvy6	caenorhabdi
928	119	4.7	791	2	Q9GK49	Q9gk49	bos taurus
929	119	4.7	841	2	Q67ZD0	Q67zd0	arabidopsis
930	119	4.7	2212	2	Q7Q112	Q7q112	anopheles g
931	119	4.7	3687	2	Q9W332	Q9w332	drosophila
932	118.5	4.7	150	2	Q65Y00	Q65y00	drosophila
933	118.5	4.7	160	2	Q86FN1	Q86fn1	caenorhabdi
934	118.5	4.7	259	2	Q93519	Q93519	caenorhabdi
935	118.5	4.7	260	2	Q7PRE8	Q7pre8	anopheles g
936	118.5	4.7	269	2	Q7Q5I2	Q7q5i2	anopheles g
937	118.5	4.7	323	1	SCGF_HUMAN	Q9y240	homo sapien
938	118.5	4.7	342	2	Q6P192	Q6p192	homo sapien
939	118.5	4.7	551	1	LEM2_RABIT	P27113	oryctolagus
940	118.5	4.7	555	2	Q9XV91	Q9xv91	caenorhabdi
941	118.5	4.7	605	2	Q7R4V2	Q7r4v2	giardia lam
942	118.5	4.7	800	2	Q9Y102	Q9y102	drosophila
943	118.5	4.7	1059	2	Q8CHF0	Q8chf0	mus musculu
944	118.5	4.7	1428	1	ATRN_MOUSE	Q9wu60	mus musculu
945	118.5	4.7	1700	1	BAR3_CHITE	Q03376	chironomus
946	118.5	4.7	3106	1	LMA2_MOUSE	Q60675	mus musculu
947	118.5	4.7	3110	1	LMA2_HUMAN	P24043	homo sapien
948	118	4.7	135	1	LECG_BOTJR	P83519	bothrops ja
949	118	4.7	140	2	Q7M462	Q7m462	cucumaria e
950	118	4.7	180	2	Q867R8	Q867r8	mytilus edu
951	118	4.7	180	2	Q867W0	Q867w0	mytilus gal
952	118	4.7	180	2	Q867Y4	Q867y4	mytilus edu
953	118	4.7	180	2	Q86M02	Q86m02	mytilus edu
954	118	4.7	180	2	Q86M04	Q86m04	mytilus gal
955	118	4.7	217	2	Q8C4F8	Q8c4f8	mus musculu
956	118	4.7	218	2	Q25462	Q25462	mytilus edu
957	118	4.7	220	2	O16854	O16854	onchocerca
958	118	4.7	261	2	Q9GM41	Q9gm41	macaca fasc
959	118	4.7	328	2	Q6BK18	Q6bk18	debaryomyce
960	118	4.7	438	1	NTG1_HUMAN	Q9y2i2	homo sapien
961	118	4.7	644	2	Q95RU0	Q95ru0	drosophila
962	118	4.7	674	2	Q6N027	Q6n027	homo sapien
963	118	4.7	684	2	Q8I498	Q8i498	cupiennius
964	118	4.7	770	2	Q9U2D5	Q9u2d5	caenorhabdi
965	118	4.7	781	2	Q92071	Q92071	gallus gall
966	118	4.7	1286	2	Q7QCT2	Q7qct2	anopheles g
967	118	4.7	2214	2	Q20219	Q20219	caenorhabdi
968	117.5	4.6	142	2	Q6DUK3	Q6duk3	marmota mon
969	117.5	4.6	151	2	Q6DKY3	Q6dky3	mesocestoid
970	117.5	4.6	156	2	Q26661	Q26661	strongyloce
971	117.5	4.6	219	2	Q8BMI5	Q8bmi5	mus musculu
972	117.5	4.6	225	2	Q7PFQ7	Q7pfq7	anopheles g
973	117.5	4.6	257	2	Q8WR38	Q8wr38	anopheles g
974	117.5	4.6	378	1	WIF1_BRARE	Q9w6f9	brachydanio
975	117.5	4.6	442	2	Q804X1	Q804x1	fugu rubrip
976	117.5	4.6	512	2	Q95RQ1	Q95rq1	drosophila
977	117.5	4.6	601	2	Q9CUT3	Q9cut3	mus musculu
978	117.5	4.6	669	2	Q922H0	Q922h0	mus musculu
979	117.5	4.6	1299	2	Q26489	Q26489	spodoptera
980	117.5	4.6	1531	1	SLT1_RAT	O88279	rattus norv

981	117.5	4.6	1801	1	LMB2_RAT	P15800	rattus norv
982	117.5	4.6	3301	1	CLR3_MOUSE	Q91zi0	mus musculu
983	117.5	4.6	3313	1	CLR3_RAT	O88278	rattus norv
984	117.5	4.6	3494	2	Q7LC53	Q7lc53	homo sapien
985	117	4.6	123	2	Q8T5W3	Q8t5w3	caenorhabdi
986	117	4.6	124	2	Q8T5X0	Q8t5x0	caenorhabdi
987	117	4.6	126	2	Q8C6F9	Q8c6f9	mus musculu
988	117	4.6	165	1	LIT1_MOUSE	P43137	mus musculu
989	117	4.6	172	2	Q8WTL2	Q8wtl2	caenorhabdi
990	117	4.6	180	2	Q86M00	Q86m00	mytilus tro
991	117	4.6	197	2	Q28008	Q28008	bos taurus
992	117	4.6	224	2	Q61970	Q61970	mus musculu
993	117	4.6	253	2	Q7PNX0	Q7pnx0	anopheles g
994	117	4.6	260	2	O97413	O97413	anopheles g
995	117	4.6	788	2	Q8SQB8	Q8sqb8	bos taurus
996	117	4.6	807	2	Q8MP01	Q8mp01	halocynthia
997	117	4.6	993	2	Q66PY1	Q66py1	mus musculu
998	117	4.6	1116	1	TIE2_BRARE	O73791	brachydanio
999	117	4.6	1799	2	Q8R0Y0	Q8r0y0	mus musculu
1000	117	4.6	2132	1	PGCA_MOUSE	Q61282	mus musculu
1001	117	4.6	2229	2	Q19853	Q19853	caenorhabdi
1002	117	4.6	3312	1	CLR3_HUMAN	Q9nyq7	homo sapien
1003	117	4.6	5141	2	Q700K0	Q700k0	rattus norv
1004	116.5	4.6	162	1	LEC3_MEGRO	P07439	megabalanus
1005	116.5	4.6	162	2	Q25459	Q25459	megabalanus
1006	116.5	4.6	190	2	Q863H3	Q863h3	bos taurus
1007	116.5	4.6	260	2	Q7PGC9	Q7pgc9	anopheles g
1008	116.5	4.6	647	2	Q7LZ69	Q7lz69	notophthalm
1009	116.5	4.6	838	2	Q9VQA9	Q9vqa9	drosophila
1010	116.5	4.6	1623	2	Q9U3U7	Q9u3u7	anopheles g
1011	116.5	4.6	1698	2	Q94438	Q94438	chironomus
1012	116.5	4.6	1798	1	LMB2_HUMAN	P55268	homo sapien
1013	116.5	4.6	4998	2	Q8CG65	Q8cg65	mus musculu
1014	116	4.6	101	2	Q8LRN1	Q8lrn1	malus domes
1015	116	4.6	161	2	Q7PFW3	Q7pfw3	anopheles g
1016	116	4.6	263	2	Q99740	Q99740	homo sapien
1017	116	4.6	321	1	FCE2_HUMAN	P06734	homo sapien
1018	116	4.6	652	2	Q8WSX1	Q8wsx1	dugesia tig
1019	116	4.6	695	2	Q8C9J2	Q8c9j2	mus musculu
1020	116	4.6	992	2	Q86UZ9	Q86uz9	homo sapien
1021	116	4.6	993	2	Q8IX30	Q8ix30	homo sapien
1022	116	4.6	1296	2	Q70HX0	Q70hx0	mus musculu
1023	116	4.6	1560	1	TENN_MOUSE	Q80z71	mus musculu
1024	116	4.6	1751	2	Q7PXF5	Q7pxf5	anopheles g
1025	115.5	4.6	123	2	Q8T5X3	Q8t5x3	caenorhabdi
1026	115.5	4.6	124	2	Q8T5W5	Q8t5w5	caenorhabdi
1027	115.5	4.6	126	2	Q8T5W4	Q8t5w4	caenorhabdi
1028	115.5	4.6	127	2	Q8T5W9	Q8t5w9	caenorhabdi
1029	115.5	4.6	127	2	Q8T5X2	Q8t5x2	caenorhabdi
1030	115.5	4.6	128	2	Q8T5W8	Q8t5w8	caenorhabdi
1031	115.5	4.6	128	2	Q8T5X1	Q8t5x1	caenorhabdi
1032	115.5	4.6	129	2	Q8T5W7	Q8t5w7	caenorhabdi
1033	115.5	4.6	129	2	Q8T5X4	Q8t5x4	caenorhabdi
1034	115.5	4.6	158	2	Q90WI6	Q90wi6	bungarus mu
1035	115.5	4.6	456	1	PRTC_CANFA	Q28278	canis famil
1036	115.5	4.6	494	2	Q8VDV0	Q8vdv0	mus musculu
1037	115.5	4.6	494	2	Q8BMS0	Q8bms0	mus musculu
1038	115.5	4.6	932	2	O57587	O57587	brachydanio
1039	115.5	4.6	1001	2	Q6ZQ64	Q6zq64	mus musculu
1040	115.5	4.6	1168	2	Q967S8	Q967s8	schistocerc
1041	115.5	4.6	2144	1	CLR2_RAT	Q9qyp2	rattus norv
1042	115	4.5	191	2	Q9DED0	Q9ded0	gallus gall
1043	115	4.5	214	2	Q9R0Q8	Q9r0q8	mus musculu
1044	115	4.5	248	2	Q9BIQ6	Q9biq6	cooperia pu
1045	115	4.5	252	2	Q9NTF1	Q9ntf1	homo sapien
1046	115	4.5	379	1	WIF1_MOUSE	Q9wua1	mus musculu
1047	115	4.5	427	2	Q6IQW7	Q6iqw7	brachydanio
1048	115	4.5	545	2	P90732	P90732	caenorhabdi
1049	115	4.5	723	2	Q9QW16	Q9qw16	rattus sp.
1050	115	4.5	816	1	NEL_CHICK	Q90827	gallus gall
1051	115	4.5	1075	2	Q9NC90	Q9nc90	strongyloce
1052	115	4.5	1785	2	Q8JHV7	Q8jhv7	brachydanio
1053	114.5	4.5	155	2	Q6Y1L9	Q6y1l9	drosophila
1054	114.5	4.5	263	2	Q7Q5I3	Q7q5i3	anopheles g
1055	114.5	4.5	400	2	Q9NT44	Q9nt44	homo sapien
1056	114.5	4.5	419	2	Q18492	Q18492	caenorhabdi
1057	114.5	4.5	579	2	Q658K9	Q658k9	homo sapien
1058	114.5	4.5	591	2	Q9P133	Q9p133	homo sapien
1059	114.5	4.5	610	1	LEM2_HORSE	Q95lg1	equus cabal
1060	114.5	4.5	628	2	Q9BZP1	Q9bzp1	homo sapien
1061	114.5	4.5	788	2	Q07012	Q07012	xenopus lae
1062	114.5	4.5	1326	2	Q13019	Q13019	homo sapien
1063	114.5	4.5	1465	2	Q13018	Q13018	homo sapien
1064	114.5	4.5	2813	2	Q6XUV6	Q6xuv6	mus musculu
1065	114.5	4.5	2813	2	Q8CIZ8	Q8ciz8	mus musculu
1066	114.5	4.5	2920	1	CLR2_MOUSE	Q9r0m0	mus musculu
1067	114	4.5	134	2	Q9XYX4	Q9xyx4	hydra oliga
1068	114	4.5	155	2	P91214	P91214	caenorhabdi
1069	114	4.5	289	2	Q20928	Q20928	caenorhabdi
1070	114	4.5	310	2	Q7V7B4	Q7v7b4	prochloroco
1071	114	4.5	379	2	Q6IN38	Q6in38	rattus norv
1072	114	4.5	413	2	Q9H8S1	Q9h8s1	homo sapien
1073	114	4.5	434	2	Q751X5	Q751x5	ashbya goss
1074	114	4.5	446	2	Q9N3X0	Q9n3x0	caenorhabdi
1075	114	4.5	628	2	Q9JI33	Q9ji33	mus musculu
1076	114	4.5	787	2	Q8R2H2	Q8r2h2	rattus norv
1077	114	4.5	799	1	ITB5_HUMAN	P18084	homo sapien
1078	114	4.5	856	2	Q8QUT7	Q8qut7	infectious
1079	114	4.5	1097	2	Q8TDW7	Q8tdw7	homo sapien
1080	114	4.5	1194	2	Q9W737	Q9w737	gallus gall
1081	114	4.5	1350	2	Q7T3T6	Q7t3t6	brachydanio
1082	114	4.5	1587	1	LMG3_HUMAN	Q9y6n6	homo sapien
1083	114	4.5	2087	2	Q8MVW7	Q8mvw7	naegleria g
1084	114	4.5	4555	2	Q8R508	Q8r508	rattus norv
1085	113.5	4.5	159	2	Q6T7B7	Q6t7b7	bitis gabon
1086	113.5	4.5	261	2	Q8T9U1	Q8t9u1	aedes aegyp
1087	113.5	4.5	468	2	Q9UC32	Q9uc32	homo sapien
1088	113.5	4.5	575	1	TRBM_HUMAN	P07204	homo sapien
1089	113.5	4.5	575	1	TRBM_SAISC	Q71u07	saimiri sci
1090	113.5	4.5	575	2	Q8IV29	Q8iv29	homo sapien
1091	113.5	4.5	619	2	Q6NWK9	Q6nwk9	brachydanio
1092	113.5	4.5	827	2	Q68FG9	Q68fg9	mus musculu
1093	113.5	4.5	1581	1	LMG3_MOUSE	Q9r0b6	mus musculu
1094	113	4.5	167	2	Q6UTX2	Q6utx2	hippocampus
1095	113	4.5	185	2	Q8WQQ3	Q8wqq3	calliphora
1096	113	4.5	191	2	Q8T5Z0	Q8t5z0	caenorhabdi
1097	113	4.5	191	2	Q8T5Z1	Q8t5z1	caenorhabdi
1098	113	4.5	193	2	Q8STG0	Q8stg0	caenorhabdi
1099	113	4.5	193	2	Q8T5Z2	Q8t5z2	caenorhabdi
1100	113	4.5	194	2	Q8T5Z3	Q8t5z3	caenorhabdi
1101	113	4.5	358	2	Q9HFZ2	Q9hfz2	candida alb
1102	113	4.5	590	2	Q8C088	Q8c088	mus musculu
1103	113	4.5	619	1	MTN4_HUMAN	O95460	homo sapien
1104	113	4.5	680	2	Q9QW15	Q9qw15	mus sp. bet
1105	113	4.5	787	1	ITB3_MOUSE	O54890	mus musculu
1106	113	4.5	788	2	Q6GP06	Q6gp06	xenopus lae
1107	113	4.5	990	2	Q6BTQ2	Q6btq2	debaryomyce
1108	113	4.5	1069	2	Q9BPS2	Q9bps2	bombyx mori
1109	113	4.5	1952	2	Q8MVW6	Q8mvw6	naegleria g
1110	113	4.5	2386	1	EFL4_HUMAN	Q7z7m0	homo sapien
1111	113	4.5	2717	2	Q94710	Q94710	paramecium
1112	113	4.5	4610	2	Q8AXB7	Q8axb7	brachydanio
1113	112.5	4.4	173	2	Q800Z5	Q800z5	salmo salar
1114	112.5	4.4	222	2	O18519	O18519	haemonchus
1115	112.5	4.4	232	2	Q7PNC5	Q7pnc5	anopheles g
1116	112.5	4.4	456	2	Q9W3W5	Q9w3w5	drosophila
1117	112.5	4.4	652	1	CD93_HUMAN	Q9npy3	homo sapien
1118	112.5	4.4	652	2	Q8IXK1	Q8ixk1	homo sapien
1119	112.5	4.4	797	2	Q7QIQ6	Q7qiq6	anopheles g
1120	112.5	4.4	799	2	Q6PE70	Q6pe70	mus musculu
1121	112.5	4.4	810	1	NEL1_HUMAN	Q92832	homo sapien
1122	112.5	4.4	810	2	Q6NSY8	Q6nsy8	homo sapien
1123	112.5	4.4	907	2	Q9XTS9	Q9xts9	caenorhabdi
1124	112.5	4.4	1191	1	LMG2_MOUSE	Q61092	mus musculu
1125	112.5	4.4	1582	2	Q8CGM0	Q8cgm0	mus musculu
1126	112.5	4.4	2731	2	Q9VJT5	Q9vjt5	drosophila

1127	112.5	4.4	2809	1	FBN3_HUMAN	Q75n90	homo sapien
1128	112.5	4.4	3367	2	Q9XZC9	Q9xzc9	drosophila
1129	112.5	4.4	3375	2	Q8IP51	Q8ip51	drosophila
1130	112	4.4	165	1	LITH_RAT	P10758	rattus norv
1131	112	4.4	179	2	O35778	O35778	rattus norv
1132	112	4.4	225	2	Q7T3M7	Q7t3m7	gallus gall
1133	112	4.4	321	2	Q9XUL7	Q9xul7	caenorhabdi
1134	112	4.4	330	2	Q6BXP9	Q6bxp9	debaryomyce
1135	112	4.4	410	2	Q7T3M8	Q7t3m8	gallus gall
1136	112	4.4	448	2	Q9VJU8	Q9vju8	drosophila
1137	112	4.4	469	2	Q9N3V9	Q9n3v9	caenorhabdi
1138	112	4.4	655	1	ITB5_PAPCY	Q07441	papio cynoc
1139	112	4.4	657	2	Q7QYH8	Q7qyh8	giardia lam
1140	112	4.4	783	2	Q90XG2	Q90xg2	gallus gall
1141	112	4.4	787	2	Q863C4	Q863c4	ovis aries
1142	112	4.4	1135	2	Q7QI37	Q7qi37	anopheles g
1143	112	4.4	1374	2	Q7QQP4	Q7qqp4	giardia lam
1144	112	4.4	1535	1	LML1_CAEEL	Q18823	caenorhabdi
1145	111.5	4.4	173	2	Q800Z7	Q800z7	salmo salar
1146	111.5	4.4	597	2	O35727	O35727	mus musculu
1147	111.5	4.4	608	2	Q80V54	Q80v54	mus musculu
1148	111.5	4.4	622	2	Q7QWD2	Q7qwd2	giardia lam
1149	111.5	4.4	643	1	CD93_RAT	Q9et61	rattus norv
1150	111.5	4.4	721	1	GAS6_HUMAN	Q14393	homo sapien
1151	111.5	4.4	1679	2	Q7QJR9	Q7qjr9	anopheles g
1152	111.5	4.4	3170	2	Q7PN80	Q7pn80	anopheles g
1153	111.5	4.4	3695	1	LMA5_HUMAN	O15230	homo sapien
1154	111.5	4.4	3695	2	Q8TDF8	Q8tdf8	homo sapien
1155	111	4.4	135	1	LECG_BITAR	Q9psn0	bitis ariet
1156	111	4.4	138	2	Q6UTY0	Q6uty0	bos taurus
1157	111	4.4	172	2	Q8WY28	Q8wy28	homo sapien
1158	111	4.4	271	2	Q9XZ44	Q9xz44	lutzomyia l
1159	111	4.4	349	2	Q7JNV6	Q7jnv6	caenorhabdi
1160	111	4.4	357	2	Q7JNV7	Q7jnv7	caenorhabdi
1161	111	4.4	375	2	Q6FH08	Q6fh08	homo sapien
1162	111	4.4	425	2	Q6PT99	Q6pt99	bos taurus
1163	111	4.4	649	2	Q6DIG3	Q6dig3	xenopus tro
1164	111	4.4	653	1	HGFA_MOUSE	Q9r098	mus musculu
1165	111	4.4	653	2	Q8VCS4	Q8vcs4	mus musculu
1166	111	4.4	815	2	Q96JS2	Q96js2	homo sapien
1167	111	4.4	816	1	NEL2_HUMAN	Q99435	homo sapien
1168	111	4.4	874	1	EPL4_RAT	Q9qyp0	rattus norv
1169	111	4.4	1050	2	Q71G60	Q71g60	red sea bre
1170	111	4.4	3034	1	CLR1_MOUSE	O35161	mus musculu
1171	111	4.4	3616	2	Q7PPF9	Q7ppf9	anopheles g
1172	110.5	4.4	158	2	Q9BYZ8	Q9byz8	homo sapien
1173	110.5	4.4	180	2	Q9TXD0	Q9txd0	mytilus edu
1174	110.5	4.4	192	2	Q7XRQ9	Q7xrq9	oryza sativ
1175	110.5	4.4	220	2	Q9UB03	Q9ub03	wuchereria
1176	110.5	4.4	236	2	Q8WUQ9	Q8wuq9	homo sapien
1177	110.5	4.4	236	2	Q7Z3S9	Q7z3s9	homo sapien
1178	110.5	4.4	291	1	EFL8_RAT	Q6mg84	rattus norv
1179	110.5	4.4	306	2	Q8C6U7	Q8c6u7	mus musculu
1180	110.5	4.4	424	2	Q8MQ79	Q8mq79	caenorhabdi
1181	110.5	4.4	502	2	O45485	O45485	caenorhabdi
1182	110.5	4.4	577	2	O35370	O35370	rattus norv
1183	110.5	4.4	594	2	Q6UY05	Q6uy05	homo sapien
1184	110.5	4.4	640	2	Q96397	Q96397	chlamydomon
1185	110.5	4.4	660	2	Q75J88	Q75j88	dictyosteli
1186	110.5	4.4	677	1	SP87_DICDI	P54643	dictyosteli
1187	110.5	4.4	798	1	ITB5_MOUSE	O70309	mus musculu
1188	110.5	4.4	837	2	Q9NAS7	Q9nas7	anopheles g
1189	110.5	4.4	871	2	Q7QE55	Q7qe55	anopheles g
1190	110.5	4.4	1292	2	Q9NJA5	Q9nja5	babesia bov
1191	110.5	4.4	1669	2	Q7Q3I9	Q7q3i9	anopheles g
1192	110	4.3	186	2	Q8MUK9	Q8muk9	strongyloce
1193	110	4.3	247	2	O44443	O44443	caenorhabdi
1194	110	4.3	277	2	Q6QH77	Q6qh77	brachydanio
1195	110	4.3	329	1	PRY2_YEAST	P36110	saccharomyc
1196	110	4.3	359	2	Q9VQX3	Q9vqx3	drosophila
1197	110	4.3	375	1	PSPD_HUMAN	P35247	homo sapien
1198	110	4.3	375	2	Q86YK9	Q86yk9	homo sapien
1199	110	4.3	465	2	Q9BIP2	Q9bip2	cooperia pu
1200	110	4.3	548	1	KUCR_MOUSE	P70194	mus musculu
1201	110	4.3	548	2	Q8BLZ8	Q8blz8	mus musculu
1202	110	4.3	798	2	Q8SQC0	Q8sqc0	bos taurus
1203	110	4.3	816	1	NEL2_RAT	Q62918	rattus norv
1204	110	4.3	816	2	Q8R417	Q8r417	rattus norv
1205	110	4.3	1369	2	Q8UW86	Q8uw86	paralichthy
1206	110	4.3	3871	2	Q20911	Q20911	caenorhabdi
1207	110	4.3	4307	2	Q19319	Q19319	caenorhabdi
1208	109.5	4.3	117	2	Q8TC19	Q8tc19	homo sapien
1209	109.5	4.3	213	2	Q6UXS8	Q6uxs8	homo sapien
1210	109.5	4.3	219	2	Q9Y0F6	Q9y0f6	thalassiosi
1211	109.5	4.3	248	1	PSPA_HUMAN	P07714	homo sapien
1212	109.5	4.3	248	2	Q8IWL1	Q8iwl1	homo sapien
1213	109.5	4.3	248	2	Q8IWL2	Q8iwl2	homo sapien
1214	109.5	4.3	251	2	Q70LQ4	Q70lq4	enchytraeus
1215	109.5	4.3	365	2	Q924Y6	Q924y6	rattus norv
1216	109.5	4.3	365	2	Q7ZRF0	Q7zrf0	chimpanzee
1217	109.5	4.3	494	2	O95965	O95965	homo sapien
1218	109.5	4.3	628	2	Q9HB63	Q9hb63	homo sapien
1219	109.5	4.3	644	1	UROM_RAT	P27590	rattus norv
1220	109.5	4.3	644	2	Q642D6	Q642d6	rattus norv
1221	109.5	4.3	692	2	Q6PDN4	Q6pdn4	mus musculu
1222	109.5	4.3	803	1	ITB1_CHICK	P07228	gallus gall
1223	109.5	4.3	1035	2	Q7QR01	Q7qr01	giardia lam
1224	109.5	4.3	1895	1	WR19_ARATH	Q9sz67	arabidopsis
1225	109.5	4.3	5146	2	Q8SPM4	Q8spm4	bos taurus
1226	109	4.3	100	2	O48632	O48632	vitis vinif
1227	109	4.3	220	2	Q99KR2	Q99kr2	mus musculu
1228	109	4.3	248	2	Q9BIQ8	Q9biq8	cooperia pu
1229	109	4.3	349	2	Q17377	Q17377	caenorhabdi
1230	109	4.3	375	2	Q8TCD8	Q8tcd8	homo sapien
1231	109	4.3	384	2	Q9Y0F7	Q9y0f7	thalassiosi
1232	109	4.3	407	2	Q95QR9	Q95qr9	caenorhabdi
1233	109	4.3	592	2	Q7R630	Q7r630	giardia lam
1234	109	4.3	593	1	GRN_HUMAN	P28799	h granulins
1235	109	4.3	654	2	Q6QNF4	Q6qnf4	canis famil
1236	109	4.3	676	2	Q7ZWL5	Q7zwl5	xenopus lae
1237	109	4.3	689	2	Q80VA2	Q80va2	mus musculu
1238	109	4.3	696	2	Q69GM1	Q69gm1	xenopus lae
1239	109	4.3	784	2	O97702	O97702	canis famil
1240	109	4.3	784	2	Q9TUN7	Q9tun7	canis famil
1241	109	4.3	784	2	Q8BM43	Q8bm43	m mus muscu
1242	109	4.3	798	2	Q9GLP0	Q9glp0	sus scrofa
1243	109	4.3	816	1	NEL2_MOUSE	Q61220	mus musculu
1244	109	4.3	819	2	Q80UM5	Q80um5	mus musculu
1245	109	4.3	851	2	Q7Q1J5	Q7q1j5	anopheles g
1246	109	4.3	858	2	Q8BM06	Q8bm06	mus musculu
1247	109	4.3	1209	2	Q80XT9	Q80xt9	mus musculu
1248	109	4.3	1442	2	Q80Z19	Q80z19	mus musculu
1249	109	4.3	1666	1	LTB4_MOUSE	Q8k4g1	mus musculu
1250	109	4.3	3460	1	RELN_HUMAN	P78509	homo sapien
1251	109	4.3	3707	1	PGBM_MOUSE	Q05793	mus musculu
1252	108.5	4.3	131	2	Q9PSM9	Q9psm9	echis carin
1253	108.5	4.3	181	2	Q962V9	Q962v9	ancylostoma
1254	108.5	4.3	305	2	Q9N028	Q9n028	macaca fasc
1255	108.5	4.3	402	2	Q9VJU9	Q9vju9	drosophila
1256	108.5	4.3	700	2	Q7TN16	Q7tn16	mus musculu
1257	108.5	4.3	700	2	Q8C0B0	Q8c0b0	mus musculu
1258	108.5	4.3	700	2	Q9WU59	Q9wu59	mus musculu
1259	108.5	4.3	787	2	Q6AYF4	Q6ayf4	rattus norv
1260	108.5	4.3	966	2	Q22378	Q22378	caenorhabdi
1261	108	4.3	231	2	Q9BIQ7	Q9biq7	cooperia pu
1262	108	4.3	240	2	Q68S97	Q68s97	salmo salar
1263	108	4.3	280	2	Q95XX2	Q95xx2	caenorhabdi
1264	108	4.3	285	2	Q8XUZ0	Q8xuz0	ralstonia s
1265	108	4.3	293	2	Q20979	Q20979	caenorhabdi
1266	108	4.3	581	2	Q9XZM7	Q9xzm7	strongyloce
1267	108	4.3	603	1	FA12_CAVPO	Q04962	cavia porce
1268	108	4.3	773	1	ITB1_BOVIN	P53712	bos taurus
1269	108	4.3	788	2	Q9TUN3	Q9tun3	oryctolagus
1270	108	4.3	803	2	Q7QSK8	Q7qsk8	giardia lam
1271	108	4.3	1431	1	SBN2_RAT	Q8cfm6	rattus norv
1272	108	4.3	1450	1	SREJ_STRPU	Q26627	strongyloce

1273	108	4.3	1476	2	Q8WRF4	Q8wrf4	monosiga br
1274	108	4.3	1486	2	O14637	O14637	homo sapien
1275	108	4.3	2327	2	Q9IBG7	Q9ibg7	xenopus lae
1276	107.5	4.3	144	2	Q6DDD6	Q6ddd6	xenopus lae
1277	107.5	4.3	166	2	Q18821	Q18821	caenorhabdi
1278	107.5	4.3	182	2	Q8WXX8	Q8wxx8	homo sapien
1279	107.5	4.3	213	2	Q8WTT0	Q8wtt0	homo sapien
1280	107.5	4.3	246	2	Q7Q756	Q7q756	anopheles g
1281	107.5	4.3	255	2	Q6TS13	Q6ts13	culex quinq
1282	107.5	4.3	293	1	EFL8_HUMAN	Q99944	homo sapien
1283	107.5	4.3	362	2	O44871	O44871	caenorhabdi
1284	107.5	4.3	491	2	Q8BJB5	Q8bjb5	mus musculu
1285	107.5	4.3	577	1	ITB6_CAVPO	P18563	cavia porce
1286	107.5	4.3	577	1	TRBM_MOUSE	P15306	mus musculu
1287	107.5	4.3	757	2	Q9HCU0	Q9hcu0	homo sapien
1288	107.5	4.3	758	2	Q6PJ75	Q6pj75	homo sapien
1289	107.5	4.3	769	1	ITB2_HUMAN	P05107	homo sapien
1290	107.5	4.3	921	2	Q6CP14	Q6cp14	kluyveromyc
1291	107.5	4.3	1271	1	YC81_CAEEL	Q19981	caenorhabdi
1292	107.5	4.3	1329	2	Q9BMB0	Q9bmb0	caenorhabdi
1293	107.5	4.3	2610	2	Q19482	Q19482	caenorhabdi
1294	107.5	4.3	3712	1	LMA_DROME	Q00174	drosophila
1295	107.5	4.3	3712	2	Q9VRW0	Q9vrw0	drosophila
1296	107.5	4.3	4543	1	LRP1_CHICK	P98157	gallus gall
1297	107	4.2	142	1	STR2_STRCA	P83515	struthio ca
1298	107	4.2	210	2	Q8BKJ4	Q8bkj4	mus musculu
1299	107	4.2	257	2	Q9VPS1	Q9vps1	drosophila
1300	107	4.2	295	2	Q9XUA7	Q9xua7	caenorhabdi
1301	107	4.2	403	2	O14549	O14549	homo sapien
1302	107	4.2	458	2	O16285	O16285	caenorhabdi
1303	107	4.2	788	1	ITB3_HUMAN	P05106	homo sapien
1304	107	4.2	1048	2	Q86KY8	Q86ky8	dictyosteli
1305	107	4.2	1696	1	PCK5_BRACL	Q9nj15	branchiosto
1306	106.5	4.2	138	2	Q7Q6T4	Q7q6t4	anopheles g
1307	106.5	4.2	142	1	OC17_CHICK	Q9prs8	gallus gall
1308	106.5	4.2	163	1	ANP_HEMAM	P05140	hemitripter
1309	106.5	4.2	176	2	Q9V9L3	Q9v913	drosophila
1310	106.5	4.2	214	1	SC14_SCHCO	P35795	schizophyll
1311	106.5	4.2	256	1	LPSB_PERAM	P26305	periplaneta
1312	106.5	4.2	257	2	Q7QYY8	Q7qyy8	giardia lam
1313	106.5	4.2	304	2	Q68S96	Q68s96	salmo salar
1314	106.5	4.2	471	2	Q804X6	Q804x6	gallus gall
1315	106.5	4.2	597	2	Q6PER0	Q6per0	mus musculu
1316	106.5	4.2	609	2	Q80YC5	Q80yc5	mus musculu
1317	106.5	4.2	655	1	HGFA_HUMAN	Q04756	homo sapien
1318	106.5	4.2	682	2	Q6ZMN9	Q6zmn9	homo sapien
1319	106.5	4.2	700	2	Q96QV1	Q96qv1	homo sapien
1320	106.5	4.2	700	2	Q9BXK3	Q9bxk3	homo sapien
1321	106.5	4.2	700	2	Q9H1J4	Q9h1j4	homo sapien
1322	106.5	4.2	799	1	ITB1_RAT	P49134	rattus norv
1323	106.5	4.2	971	2	Q6ZWI1	Q6zwi1	homo sapien
1324	106.5	4.2	999	2	Q9NQ36	Q9nq36	homo sapien
1325	106.5	4.2	1222	2	Q7PPC0	Q7ppc0	anopheles g
1326	106.5	4.2	4590	1	FATH_HUMAN	Q14517	homo sapien
1327	106	4.2	189	2	Q86LZ9	Q86lz9	mytilus edu
1328	106	4.2	227	1	NK11_MOUSE	P27811	mus musculu
1329	106	4.2	227	2	Q91V25	Q91v25	mus musculu
1330	106	4.2	238	1	209A_MOUSE	Q91zx1	mus musculu
1331	106	4.2	255	2	Q64HY2	Q64hy2	oncorhynchu
1332	106	4.2	293	2	Q6UXB4	Q6uxb4	homo sapien
1333	106	4.2	369	2	Q863A1	Q863a1	bos taurus
1334	106	4.2	438	2	Q68FE5	Q68fe5	mus musculu
1335	106	4.2	470	2	Q69ZU3	Q69zu3	mus musculu
1336	106	4.2	491	2	Q9BIQ4	Q9biq4	cooperia pu
1337	106	4.2	615	1	FA12_HUMAN	P00748	homo sapien
1338	106	4.2	615	2	Q8IZZ5	Q8izz5	homo sapien
1339	106	4.2	652	2	Q8WSX0	Q8wsx0	dugesia tig
1340	106	4.2	735	2	O95784	O95784	homo sapien
1341	106	4.2	765	2	Q91V98	Q91v98	mus musculu
1342	106	4.2	765	2	Q91ZV1	Q91zv1	mus musculu
1343	106	4.2	858	2	Q7PS95	Q7ps95	anopheles g
1344	106	4.2	887	2	Q7ZBS0	Q7zbs0	chimpanzee
1345	106	4.2	937	2	Q9BLJ1	Q9blj1	ciona intes
1346	106	4.2	1260	2	Q7ZYV5	Q7zyv5	oncorhynchu
1347	106	4.2	1576	1	YLK3_CAEEL	P41951	caenorhabdi
1348	106	4.2	1761	2	Q86XN2	Q86xn2	homo sapien
1349	106	4.2	1827	2	Q20535	Q20535	caenorhabdi
1350	106	4.2	1842	1	LTB2_BOVIN	Q28019	bos taurus
1351	106	4.2	1969	2	Q69HL6	Q69hl6	ciona intes
1352	106	4.2	2517	2	Q7QL19	Q7ql19	anopheles g
1353	106	4.2	3672	1	LML2_CAEEL	Q21313	caenorhabdi
1354	106	4.2	3704	2	P91904	P91904	caenorhabdi
1355	105.5	4.2	122	2	Q869J5	Q869j5	archispiros
1356	105.5	4.2	160	2	O18076	O18076	caenorhabdi
1357	105.5	4.2	173	2	Q800Z6	Q800z6	salmo salar
1358	105.5	4.2	256	2	Q20043	Q20043	caenorhabdi
1359	105.5	4.2	259	2	Q8I6R0	Q8i6r0	anopheles s
1360	105.5	4.2	270	2	Q7QF84	Q7qf84	anopheles g
1361	105.5	4.2	283	1	LECA_SARPE	P05047	sarcophaga
1362	105.5	4.2	287	2	Q8MVJ7	Q8mvj7	boltenia vi
1363	105.5	4.2	342	2	Q9TXW7	Q9txw7	caenorhabdi
1364	105.5	4.2	810	1	NEL1_RAT	O62919	rattus norv
1365	105.5	4.2	1117	2	Q6E0K3	Q6e0k3	didelphis m
1366	105.5	4.2	1522	1	BAI3_HUMAN	O60242	homo sapien
1367	105.5	4.2	3718	1	LMA5_MOUSE	Q61001	mus musculu
1368	105	4.2	112	2	Q9H557	Q9h557	homo sapien
1369	105	4.2	160	2	Q9ZPG2	Q9zpg2	arabidopsis
1370	105	4.2	227	2	Q925G4	Q925g4	mus musculu
1371	105	4.2	255	2	Q68S98	Q68s98	salmo salar
1372	105	4.2	378	2	Q21756	Q21756	caenorhabdi
1373	105	4.2	463	1	MFGM_MOUSE	P21956	mus musculu
1374	105	4.2	540	2	Q800Y7	Q800y7	meleagris g
1375	105	4.2	582	2	Q7QPM3	Q7qpm3	giardia lam
1376	105	4.2	642	2	Q91X17	Q91x17	mus musculu
1377	105	4.2	961	1	TSP4_HUMAN	P35443	homo sapien
1378	105	4.2	1373	2	O75372	O75372	homo sapien
1379	105	4.2	2448	2	Q8WWQ5	Q8wwq5	homo sapien
1380	104.5	4.1	124	2	Q8T5W6	Q8t5w6	caenorhabdi
1381	104.5	4.1	152	2	Q8C1G3	Q8c1g3	mus musculu
1382	104.5	4.1	199	2	Q6SPF9	Q6spf9	tribolium c
1383	104.5	4.1	204	2	Q95X90	Q95x90	caenorhabdi
1384	104.5	4.1	223	2	O02255	O02255	caenorhabdi
1385	104.5	4.1	238	2	Q9QZ15	Q9qz15	m dendritic
1386	104.5	4.1	241	2	Q7Q5H1	Q7q5h1	anopheles g
1387	104.5	4.1	253	2	Q6XYD1	Q6xyd1	homo sapien
1388	104.5	4.1	262	2	Q923C7	Q923c7	mus musculu
1389	104.5	4.1	269	2	Q7PPX0	Q7ppx0	anopheles g
1390	104.5	4.1	332	2	Q8JZN1	Q8jzn1	mus musculu
1391	104.5	4.1	356	2	Q22913	Q22913	caenorhabdi
1392	104.5	4.1	375	2	Q6PHH2	Q6phh2	brachydanio
1393	104.5	4.1	427	1	MFGM_RAT	P70490	rattus norv
1394	104.5	4.1	454	2	Q9NAK6	Q9nak6	caenorhabdi
1395	104.5	4.1	504	2	Q7QWR4	Q7qwr4	giardia lam
1396	104.5	4.1	814	2	Q7ZXL5	Q7zxl5	xenopus lae
1397	104.5	4.1	1174	2	Q99K58	Q99k58	mus musculu
1398	104.5	4.1	1221	1	FBL2_MOUSE	P37889	mus musculu
1399	104.5	4.1	1821	1	LTB2_HUMAN	Q14767	homo sapien
1400	104.5	4.1	1821	2	Q6AZ94	Q6az94	homo sapien
1401	104.5	4.1	3646	2	Q7Q737	Q7q737	anopheles g
1402	104	4.1	181	2	Q6BHZ7	Q6bhz7	debaryomyce
1403	104	4.1	380	2	O02343	O02343	caenorhabdi
1404	104	4.1	415	2	O16660	O16660	caenorhabdi
1405	104	4.1	581	2	Q8NAV8	Q8nav8	homo sapien
1406	104	4.1	624	1	MTN4_MOUSE	O89029	mus musculu
1407	104	4.1	704	2	O74567	O74567	trichoderma
1408	104	4.1	784	2	Q95JH1	Q95jh1	sus scrofa
1409	104	4.1	784	2	Q9TUN5	Q9tun5	sus scrofa
1410	104	4.1	788	2	O96444	O96444	biomphalari
1411	104	4.1	809	1	PAT3_CAEEL	Q27874	caenorhabdi
1412	104	4.1	862	2	Q9UF98	Q9uf98	homo sapien
1413	104	4.1	880	2	Q8NAU9	Q8nau9	homo sapien
1414	104	4.1	1136	2	Q7QPZ3	Q7qpz3	giardia lam
1415	104	4.1	1725	2	P70570	P70570	rattus norv
1416	104	4.1	1914	2	Q91008	Q91008	gallus gall
1417	104	4.1	2447	2	Q9NEF9	Q9nef9	drosophila
1418	104	4.1	2551	1	SBN2_HUMAN	Q8wwq8	h stabilin

1419	104	4.1	3215	2	Q8IRV7	Q8irv7 drosophila
1420	104	4.1	3775	2	Q7PMF9	Q7pmf9 anopheles g
1421	104	4.1	4117	2	Q8IRV9	Q8irv9 drosophila
1422	104	4.1	4179	2	Q9W4Y4	Q9w4y4 drosophila
1423	104	4.1	4223	2	Q8MPN3	Q8mpn3 drosophila
1424	104	4.1	4228	2	Q8IRV8	Q8irv8 drosophila
1425	104	4.1	5376	1	ZAN_MOUSE	O88799 mus musculu
1426	103.5	4.1	154	2	Q800Z3	Q800z3 salmo salar
1427	103.5	4.1	251	2	Q24774	Q24774 enchytraeus
1428	103.5	4.1	284	2	Q9VJU6	Q9vju6 drosophila
1429	103.5	4.1	299	2	Q869J8	Q869j8 glomeris ma
1430	103.5	4.1	369	1	PSPD_BOVIN	P35246 bos taurus
1431	103.5	4.1	379	2	O45528	O45528 caenorhabdi
1432	103.5	4.1	448	2	Q6UWA3	Q6uwa3 homo sapien
1433	103.5	4.1	612	2	Q6ZQ96	Q6zq96 mus musculu
1434	103.5	4.1	749	2	Q86TP7	Q86tp7 homo sapien
1435	103.5	4.1	762	2	Q7YVQ5	Q7yvq5 trypanosoma
1436	103.5	4.1	768	1	ITB8_RABIT	P26013 oryctolagus
1437	103.5	4.1	772	2	Q9PUU4	Q9puu4 ictalurus p
1438	103.5	4.1	813	1	YTQJ_CAEEL	Q19673 caenorhabdi
1439	103.5	4.1	952	2	Q8I7T3	Q8i7t3 dictyosteli
1440	103.5	4.1	1026	2	Q8SWY0	Q8swy0 drosophila
1441	103.5	4.1	1193	1	LMG2_HUMAN	Q13753 homo sapien
1442	103.5	4.1	1282	2	Q68FL1	Q68fl1 mus musculu
1443	103.5	4.1	1296	2	Q6AWM6	Q6awm6 drosophila
1444	103.5	4.1	1522	1	BAI3_MOUSE	Q80zf8 mus musculu
1445	103.5	4.1	1790	1	LMB1_DROME	P11046 drosophila
1446	103	4.1	162	2	Q6UTX1	Q6utx1 hippocampus
1447	103	4.1	178	1	209C_MOUSE	Q91zw9 mus musculu
1448	103	4.1	227	2	Q61973	Q61973 mus musculu
1449	103	4.1	293	2	Q8R188	Q8r188 mus musculu
1450	103	4.1	294	2	Q8BNX1	Q8bnx1 mus musculu
1451	103	4.1	401	2	Q811K6	Q811k6 mus musculu
1452	103	4.1	498	2	Q66NE4	Q66ne4 bombyx mori
1453	103	4.1	510	2	Q9H4V1	Q9h4v1 homo sapien
1454	103	4.1	612	1	LEM2_MOUSE	Q00690 mus musculu
1455	103	4.1	684	2	Q9BIM7	Q9bim7 toxoplasma
1456	103	4.1	758	2	Q66NE3	Q66ne3 bombyx mori
1457	103	4.1	768	2	Q98TH8	Q98th8 cyprinus ca
1458	103	4.1	783	2	Q9Y0F8	Q9y0f8 thalassiosi
1459	103	4.1	788	1	ITB6_HUMAN	P18564 homo sapien
1460	103	4.1	848	2	Q8C720	Q8c720 mus musculu
1461	103	4.1	921	2	Q7PFW4	Q7pfw4 anopheles g
1462	103	4.1	1116	2	Q07898	Q07898 homo sapien
1463	103	4.1	1149	2	Q07901	Q07901 homo sapien
1464	103	4.1	1151	2	Q07899	Q07899 homo sapien
1465	103	4.1	1156	2	Q07900	Q07900 homo sapien
1466	103	4.1	1156	2	Q86VB7	Q86vb7 homo sapien
1467	103	4.1	1537	2	Q7KSH7	Q7ksh7 drosophila
1468	103	4.1	1630	2	Q6PCS0	Q6pcs0 mus musculu
1469	103	4.1	1688	2	Q8SXB0	Q8sxb0 drosophila
1470	102.5	4.1	149	2	Q8UVC7	Q8uvc7 agkistrodon
1471	102.5	4.1	272	2	Q7PZ79	Q7pz79 anopheles g
1472	102.5	4.1	443	2	Q8JHC9	Q8jhc9 brachydanio
1473	102.5	4.1	458	1	PRTC_RABIT	Q28661 oryctolagus
1474	102.5	4.1	461	1	PRTC_HUMAN	P04070 homo sapien
1475	102.5	4.1	722	2	Q7KWS7	Q7kws7 dictyosteli
1476	102.5	4.1	733	2	Q86VG1	Q86vg1 homo sapien
1477	102.5	4.1	736	2	Q6ZNB6	Q6znb6 homo sapien
1478	102.5	4.1	737	2	Q6IR63	Q6ir63 xenopus lae
1479	102.5	4.1	741	2	Q96K89	Q96k89 homo sapien
1480	102.5	4.1	798	1	ITB1_HUMAN	P05556 homo sapien
1481	102.5	4.1	798	1	ITB1_MOUSE	P09055 mus musculu
1482	102.5	4.1	798	2	Q8WUM6	Q8wum6 homo sapien
1483	102.5	4.1	798	2	Q8BTU0	Q8btu0 mus musculu
1484	102.5	4.1	806	2	O61677	O61677 lytechinus
1485	102.5	4.1	823	2	Q7Z3V1	Q7z3v1 homo sapien
1486	102.5	4.1	915	2	O02364	O02364 caenorhabdi
1487	102.5	4.1	927	2	Q7JKS6	Q7jks6 caenorhabdi
1488	102.5	4.1	943	1	BLI4_CAEEL	P51559 caenorhabdi
1489	102.5	4.1	1188	2	Q9SY59	Q9sy59 arabidopsis
1490	102.5	4.1	1224	2	Q7T024	Q7t024 brachydanio
1491	102.5	4.1	1244	2	Q69YJ3	Q69yj3 homo sapien
1492	102.5	4.1	1519	2	Q8WPN0	Q8wpn0 oikopleura
1493	102.5	4.1	1766	2	Q8AW45	Q8aw45 brachydanio
1494	102.5	4.1	2673	2	Q96SC3	Q96sc3 homo sapien
1495	102.5	4.1	4283	2	Q9ERV0	Q9erv0 rattus norv
1496	102.5	4.1	5636	2	Q96RW7	Q96rw7 homo sapien
1497	102	4.0	146	2	Q9VQA7	Q9vqa7 drosophila
1498	102	4.0	166	2	Q90WJ8	Q90wj8 anguilla ja
1499	102	4.0	200	2	Q802S8	Q802s8 gallus gall
1500	102	4.0	467	2	Q86WX2	Q86wx2 homo sapien

ALIGNMENTS

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RESULT 1
Q6UXF7
ID   Q6UXF7      PRELIMINARY;      PRT;   455 AA.
AC   Q6UXF7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   LHPE306.
GN   ORFNames=UNQ306;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
CC   -!- SIMILARITY: Contains 2 EGF-like domains.
DR   EMBL; AY358373; AAQ88739.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00837; V5TPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00034; CLECT; 1.
DR   SMART; SM00181; EGF; 2.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS50026; EGF_3; 1.
KW   EGF-like domain.
SQ   SEQUENCE   455 AA;  50478 MW;  01DD09C9A23875D2 CRC64;

  Query Match           100.0%;  Score 2529;  DB 2;  Length 455;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-189;
  Matches  455;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db          1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60

Qy         61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120

Qy        121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180

Qy        181 AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240

Qy        241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300

Qy        301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT 360

Qy        361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420

Qy        421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
              |||||||||||||||||||||||||||||||||||
Db        421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
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RESULT 2
Q7Z5K9
ID   Q7Z5K9      PRELIMINARY;      PRT;   446 AA.
AC   Q7Z5K9;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Unnamed secretory protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ding P., Han W., Rui M., Wang Y., Zhang Y., Song Q., Ma D.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 2 EGF-like domains.
DR   EMBL; AF521893; AAP80866.1; -.
DR   HSSP; P04284; 1CFE.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   Pfam; PF00188; SCP; 1.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00034; CLECT; 1.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS50026; EGF_3; 1.
KW   EGF-like domain.
SQ   SEQUENCE   446 AA;  49574 MW;  EF34732BF9ECD0C1 CRC64;

  Query Match           96.4%;  Score 2438.5;  DB 2;  Length 446;
  Best Local Similarity  96.7%;  Pred. No. 4.4e-182;
  Matches  440;  Conservative    1;  Mismatches    5;  Indels    9;  Gaps    1;

Qy          1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MLHPETSPGRGHLLAVLLALLGTAWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60

Qy         61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         61 WVQPPAADMRRLDWSDSLAQLAQARAALCGTPTPSLASGLWRTLQVGWNMQLLPAGLASF 120

Qy        121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQAAIEAFVC 180

Qy        181 AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240
              ||||  |||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        181 AYSPRGNWEVNGKTIVPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240

Qy        241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300

Qy        301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVI 360

Qy        361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNH---------GFGNCVEL 411

Qy        421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
              |||||||||||||||||||||||||||||||||||
Db        412 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 446
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RESULT 3
Q8NCF0
ID   Q8NCF0      PRELIMINARY;      PRT;   446 AA.
AC   Q8NCF0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein FLJ90292.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA   Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA   Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA   Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 2 EGF-like domains.
DR   EMBL; AK074773; BAC11199.1; -.
DR   HSSP; P04284; 1CFE.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00837; V5TPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00034; CLECT; 1.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
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DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS50026; EGF_3; 1.
KW   EGF-like domain.
SQ   SEQUENCE   446 AA;  49557 MW;  99B5ED7BC71A6DE2 CRC64;

  Query Match             95.9%;  Score 2426.5;  DB 2;  Length 446;
  Best Local Similarity   96.3%;  Pred. No. 3.8e-181;
  Matches  438;  Conservative    2;  Mismatches    6;  Indels    9;  Gaps    1;

Qy          1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db          1 MLHPETSPGRGHLLAVLLALLGTAWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60

Qy         61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120
              |||||||||||||||||||||||||||| |||||||| ||||||||||||||||||||
Db         61 WVQPPAADMRRLDWSDSLAQLAQARAALCGTPTPSLASGPWRTLQVGWNMQLLPAGLASF 120

Qy        121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQAAIEAFVC 180

Qy        181 AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240
              |||| |||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        181 AYSPRGNWEVNGKTIVPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240

Qy        241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300

Qy        301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVI 360

Qy        361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420
              |||||||||||||||||||||||||||||||||||||||||||||  |||||||| ||||||||
Db        361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNH---------GFGNCVEL 411

Qy        421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
              |||||||||:|||||||||||||||||||||||||
Db        412 QASAAFNWNNQRCKTRNRYICQFAQEHISRWGPGS 446


RESULT 4
Q6DCB3
ID   Q6DCB3      PRELIMINARY;      PRT;   446 AA.
AC   Q6DCB3;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Secretory protein LOC348174.
GN   Name=LOC348174;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Colon;
RA   Strausberg R.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 2 EGF-like domains.
DR   EMBL; BC078143; AAH78143.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00837; V5TPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00034; CLECT; 1.
DR   SMART; SM00181; EGF; 2.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS50026; EGF_3; 1.
KW   EGF-like domain.
SQ   SEQUENCE   446 AA;  49567 MW;  D936C28FB62FF33C CRC64;

  Query Match             95.8%;  Score 2423.5;  DB 2;  Length 446;
  Best Local Similarity   96.0%;  Pred. No. 6.5e-181;
  Matches  437;  Conservative    2;  Mismatches    7;  Indels    9;  Gaps    1;

Qy          1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
              |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db          1 MLHPETSPGRGHLLAVLLALLGTAWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60

Qy         61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120
              |||||||||||||||||||||||||||| |||||||||||||||||||||||||||| ||
Db         61 WVQPPAADMRRLDWSDSLAQLAQARAALCGTPTPSLASGLWRTLQVGWNMQLLPAGLVSF 120

Qy        121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQAAIEAFVC 180

Qy        181 AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240
              |||| |||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        181 AYSPRGNWEVNGKTIVPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240

Qy        241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRLREEECSCVCDIGYGGAQCATKVHFPFH 300

Qy        301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVI 360

Qy        361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVEL 420
              |||||||||||||||||||||||||||||||||||||||||||||  |||||||| ||||||||
Db        361 DSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNH---------GFGNCVEL 411

Qy        421 QASAAFNWNDQRCKTRNRYICQFAQEHISRWGPGS 455
              |||||||||:|||||||||||||||||||||||||
Db        412 QASAAFNWNNQRCKTRNRYICQFAQEHISRWGPGS 446
```

```
RESULT 5
Q7TSP9
ID   Q7TSP9      PRELIMINARY;      PRT;   473 AA.
AC   Q7TSP9;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mannose receptor-like isoform 6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA   Jang J.S. Sr., Ackerman S.L.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 2 EGF-like domains.
DR   EMBL; AY223873; AAP22987.1; -.
DR   HSSP; P04284; 1CFE.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   Pfam; PF00188; SCP; 1.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00034; CLECT; 1.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS50026; EGF_3; 1.
KW   EGF-like domain; Receptor.
SQ   SEQUENCE   473 AA;  52563 MW;  707C43A6B3C2E206 CRC64;

  Query Match           76.4%;  Score 1932.5;  DB 2;  Length 473;
  Best Local Similarity   76.4%;  Pred. No. 1.5e-142;
  Matches  352;  Conservative   33;  Mismatches   59;  Indels   17;  Gaps    4;

Qy          1 MLHPETSPGRGH------LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSL 54
              |: || |  |        || :||:||| || || |||  :| |   ||:||||||:|:
Db         22 MIQPEPSLWLGSQSRWLGLLLLLLSLLGITWTEVQPPQ-PKQDPTLQALSRKESFLILTA 80

Qy         55 HNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIP-TPSLASGLWRTLQVGWNMQLL 113
              |||||| | ||||:|:|:|||:|||||||:|||||    ||:|||       ||||:||:
Db         81 HNRLRSRVHPPAANMQRMDWSESLAQLAEARAALCVTSVTPNLASTPGHNSHVGWNVQLM 140

Qy        114 PAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQT 173
              | | |||||||:|||||| :| |   ||| |||| ||||||||||||||||  |   |
Db        141 PMGSASFVEVVNLWFAEGLQYRHGDAECAHNATCAHYTQLVWATSSQLGCGRQPCFVDQE 200

Qy        174 AIEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCR 233
              |:||||||||||||::||||: ||||| ||||||| ||||||||||||||||||||||||
Db        201 AMEAFVCAYSPGGNWDINGKTVAPYKKGTWCSLCTARVSGCFKAWDHAGGLCEVPRNPCR 260

Qy        234 MSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCAT 293
              |||:| | |||||| ||| |||||||||||||:|||||:|||:|||||:||:|||||||||
Db        261 MSCRNLGHLNISTCRCHCQPGYTGRYCQVRCSVQCVHGQFRKEECSCICDVGYGGAQCAT 320

Qy        294 KVHFPFHTCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRL 353
              || |||||||||||||||||| |||||| |:|||| ||||||||:|||||||||||||||
Db        321 KVGFPFHTCDLRIDGDCFMVSPEADTYYGAKMKCQGKGGVLAQIESQKVQDILAFYLGRL 380

Qy        354 ETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMG 413
              ||||||||||||:|||||||| ||||||| |||||:|||||||||||           |
Db        381 ETTNEVTDSDFETKNFWIGLTYKAAKDSFRWTTGEHQSFTSFAFGQPDN---------QG 431

Qy        414 FGNCVELQASAAFNWNDQRCKTRNRYICQFAQEHISRWGPG 454
              ||||||:|||||||||||||||||||||||:| ||| ||
Db        432 FGNCVEMQASAAFNWNDQRCKTRNRYICQFAQKHYSRWEPG 472


RESULT 6
Q7TSQ0
ID   Q7TSQ0      PRELIMINARY;      PRT;   504 AA.
AC   Q7TSQ0;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mannose receptor-like isoform 4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA   Jang J.S. Sr., Ackerman S.L.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 2 EGF-like domains.
DR   EMBL; AY223871; AAP22985.1; -.
DR   HSSP; P04284; 1CFE.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   Pfam; PF00188; SCP; 1.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00034; CLECT; 1.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS50026; EGF_3; 1.
KW   EGF-like domain; Receptor.
SQ   SEQUENCE   504 AA;  55995 MW;  A964C0C319D77B8C CRC64;

  Query Match           76.4%;  Score 1932.5;  DB 2;  Length 504;
  Best Local Similarity   76.4%;  Pred. No. 1.6e-142;
  Matches  352;  Conservative   33;  Mismatches   59;  Indels   17;  Gaps    4;

Qy          1 MLHPETSPGRGH------LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSL 54
              |: || |  |        || :||:||| || || |||  :| |   ||:||||||:|:
Db         53 MIQPEPSLWLGSQSRWLGLLLLLLSLLGITWTEVQPPQ-PKQDPTLQALSRKESFLILTA 111

Qy         55 HNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIP-TPSLASGLWRTLQVGWNMQLL 113
              |||||| | ||||:|:|:|||:|||||||:||||||    ||:|||       ||||:||:
Db        112 HNRLRSRVHPPAANMQRMDWSESLAQLAEARAALCVTSVTPNLASTPGHNSHVGWNVQLM 171

Qy        114 PAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQT 173
              | | |||||||:|||||| :| |   ||| |||| ||||||||||||||||  |   |
Db        172 PMGSASFVEVVNLWFAEGLQYRHGDAECAHNATCAHYTQLVWATSSQLGCGRQPCFVDQE 231

Qy        174 AIEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCR 233
              |:||||||||||||::||||: ||||| ||||||| ||||||||||||||||||||||||
Db        232 AMEAFVCAYSPGGNWDINGKTVAPYKKGTWCSLCTARVSGCFKAWDHAGGLCEVPRNPCR 291

Qy        234 MSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCAT 293
              |||:| | |||||| ||| |||||||||||||:|||||:|||:|||||:||:|||||||||
Db        292 MSCRNLGHLNISTCRCHCQPGYTGRYCQVRCSVQCVHGQFRKEECSCICDVGYGGAQCAT 351
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Qy        294 KVHFPFHTCDLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRL 353
              || |||||||||||||||||| |||||| |:|||| ||||||||:|||||||||||||||
Db        352 KVGFPFHTCDLRIDGDCFMVSPEADTYYGAKMKCQGKGGVLAQIESQKVQDILAFYLGRL 411

Qy        354 ETTNEVTDSDFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMG 413
              |||||||||||||:|||||||| ||||||| ||||||:|||||||||||          |
Db        412 ETTNEVTDSDFETKNFWIGLTYKAAKDSFRWTTGEHQSFTSFAFGQPDN---------QG 462

Qy        414 FGNCVELQASAAFNWNDQRCKTRNRYICQFAQEHISRWGPG 454
              |||||||:|||||||||||||||||||||||:| ||| ||
Db        463 FGNCVEMQASAAFNWNDQRCKTRNRYICQFAQKHYSRWEPG 503


RESULT 7
Q7TSQ7
ID   Q7TSQ7      PRELIMINARY;      PRT;   477 AA.
AC   Q7TSQ7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mannose receptor-like.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA   Jang J.S., Ackerman S.L.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 2 EGF-like domains.
DR   EMBL; AY223868; AAP20650.1; -.
DR   HSSP; P04284; 1CFE.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   Pfam; PF00188; SCP; 1.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00034; CLECT; 1.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS50026; EGF_3; 1.
KW   EGF-like domain; Receptor.
SQ   SEQUENCE   477 AA;  52490 MW;  E24C5071B4137148 CRC64;

  Query Match             73.9%;  Score 1869.5;  DB 2;  Length 477;
  Best Local Similarity   75.0%;  Pred. No. 1.2e-137;
  Matches  339;  Conservative   31;  Mismatches   49;  Indels   33;  Gaps    4;

Qy          4 PETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQ 63
              |  |  | :||:             |||          ||:|||||:|: |||||| |
Db         57 PGASGHRPNLLS------------WPP----------ALSRKESFLILTAHNRLRSRVH 93

Qy         64 PPAADMRRLDWSDSLAQLAQARAALCGIP-TPSLASGLWRTLQVGWNMQLLPAGLASFVE 122
              ||||:|:|:|||:||||||:||||||    ||:|||       ||||:||:| | |||||
Db         94 PPAANMQRMDWSESLAQLAEARAALCVTSVTPNLASTPGHNSHVGWNVQLMPMGSASFVE 153

Qy        123 VVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAY 182
              ||:|||||| :| |   ||| |||| ||||||||||||||||  |    | |:|||||||
Db        154 VVNLWFAEGLQYRHGDAECAHNATCAHYTQLVWATSSQLGCGRQPCFVDQEAMEAFVCAY 213

Qy        183 SPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRL 242
              ||||||::||||: ||||| ||||||| |||||||||||||||||||||||:| | |
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Db        214 SPGGNWDINGKTVAPYKKGTWCSLCTARVSGCFKAWDHAGGLCEVPRNPCRMSCRNLGHL 273

Qy        243 NISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHPPFHTC 302
              ||||| ||| |||||||||||||:|||||:||:|||||:||:|||||||||| ||||||
Db        274 NISTCRCHCQPGYTGRYCQVRCSVQCVHGQFRKEECSCICDVGYGGAQCATKVGPPFHTC 333

Qy        303 DLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDS 362
              |||||||||| |||||| |:|||| ||||||||:|||||||||||||||||||||||||
Db        334 DLRIDGDCFMVSPEADTYYGAKMKCQGKGGVLAQIESQKVQDILAFYLGRLETTNEVTDS 393

Qy        363 DFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQA 422
              ||||:|||||||| ||||||| |||||:|||||||||          |||||||:||
Db        394 DFETKNFWIGLTYKAAKDSFRWTTGEHQSFTSFAFGQPDN---------QGFGNCVEMQA 444

Qy        423 SAAFNWNDQRCKTRNRYICQFAQEHISRWGPG 454
              |||||||||||||||||||||||:| ||| ||
Db        445 SAAFNWNDQRCKTRNRYICQFAQKHYSRWEPG 476


RESULT 8
Q7TSQ1
ID   Q7TSQ1      PRELIMINARY;      PRT;   534 AA.
AC   Q7TSQ1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mannose receptor-like isoform 2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA   Jang J.S. Sr., Ackerman S.L.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 2 EGF-like domains.
DR   EMBL; AY223869; AAP22983.1; -.
DR   HSSP; P04284; 1CFE.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006210; IEGF.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   Pfam; PF00188; SCP; 1.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00034; CLECT; 1.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS50026; EGF_3; 1.
KW   EGF-like domain; Receptor.
SQ   SEQUENCE   534 AA;  58585 MW;  9B0AF013370793FF CRC64;

  Query Match             73.9%;  Score 1869.5;  DB 2;  Length 534;
  Best Local Similarity   75.0%;  Pred. No. 1.4e-137;
  Matches  339;  Conservative   31;  Mismatches   49;  Indels   33;  Gaps    4;

Qy          4 PETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQ 63
              |  |  | :||:             |||          ||:|||||:|: |||||| |
Db        114 PGASGHRPNLLS------------WPP----------ALSRKESFLILTAHNRLRSRVH 150

Qy         64 PPAADMRRLDWSDSLAQLAQARAALCGIP-TPSLASGLWRTLQVGWNMQLLPAGLASFVE 122
              ||||:|:|:|||:||||||:||||||    ||:|||       ||||:||:| | |||||
Db        151 PPAANMQRMDWSESLAQLAEARAALCVTSVTPNLASTPGHNSHVGWNVQLMPMGSASFVE 210
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Qy        123 VVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAY 182
              ||:|||||| :| |   ||| |||| |||||||||||||||||  |    | |:|||||||
Db        211 VVNLWFAEGLQYRHGDAECAHNATCAHYTQLVWATSSQLGCGRQPCFVDQEAMEAFVCAY 270

Qy        183 SPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRL 242
              ||||||::||||: ||||| ||||||| |||||||||||||||||||||||||:| | |
Db        271 SPGGNWDINGKTVAPYKKGTWCSLCTARVSGCFKAWDHAGGLCEVPRNPCRMSCRNLGHL 330

Qy        243 NISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTC 302
              ||||| ||| |||||||||||||:|||||:||:|||||:||:|||||||||||| ||||||
Db        331 NISTCRCHCQPGYTGRYCQVRCSVQCVHGQFRKEECSCICDVGYGGAQCATKVGFPFHTC 390

Qy        303 DLRIDGDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDS 362
              |||||||||||| |||||| |:|||| ||||||||:|||||||||||||||||||||||||
Db        391 DLRIDGDCFMVSPEADTYYGAKMKCQGKGGVLAQIESQKVQDILAFYLGRLETTNEVTDS 450

Qy        363 DFETRNFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQA 422
              ||||:|||||||-|| |||||||| |||||:||||||||||          |||||||:||
Db        451 DFETKNFWIGLTYKAAKDSFRWTTGEHQSFTSFAFGQPDN---------QGFGNCVEMQA 501

Qy        423 SAAFNWNDQRCKTRNRYICQFAQEHISRWGPG 454
              |||||||||||||||||||||:| ||| ||
Db        502 SAAFNWNDQRCKTRNRYICQFAQKHYSRWEPG 533
```

RESULT 9
Q7TMA7
ID Q7TMA7 PRELIMINARY; PRT; 379 AA.
AC Q7TMA7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mannose receptor-like isoform 3 (Mannose receptor-like isoform
DE 5).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Jang J.S. Sr., Ackerman S.L.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
DR EMBL; AY223870; AAP22984.1; -.
DR EMBL; AY223872; AAP22986.1; -.
DR HSSP; P04284; 1CFE.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS50026; EGF_3; 1.
KW EGF-like domain; Receptor.
SQ SEQUENCE 379 AA; 42164 MW; 98D94076795F85D5 CRC64;

  Query Match 69.5%; Score 1758; DB 2; Length 379;
  Best Local Similarity 80.4%; Pred. No. 4.9e-129;
  Matches 311; Conservative 25; Mismatches 41; Indels 10; Gaps 2;

```
Qy         69 MRRLDWSDSLAQLAQARAALCGIP-TPSLASGLWRTLQVGWNMQLLPAGLASFVEVVSLW 127
              |:|:|||:||||||:||||||    ||:|||       ||||:||:| | |||||||:||
Db          1 MQRMDWSESLAQLAEARAALCVTSVTPNLASTPGHNSHVGWNVQLMPMGSASFVEVVNLW  60

Qy        128 FAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPGGN 187
              |||| :| |   ||| |||| |||||||||||||||||  |    | |:|||||||||||
Db         61 FAEGLQYRHGDAECAHNATCAHYTQLVWATSSQLGCGRQPCFVDQEAMEAFVCAYSPGGN 120

Qy        188 WEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTC 247
              |::|||: ||||| ||||||| |||||||||||||||||||||||||:| | ||||||
Db        121 WDINGKTVAPYKKGTWCSLCTARVSGCFKAWDHAGGLCEVPRNPCRMSCRNLGHLNISTC 180

Qy        248 HCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRID 307
              ||| |||||||||||||:|||||:||:|||||:||:|||||||||| ||||||||||
Db        181 RCHCQPGYTGRYCQVRCSVQCVHGQFRKEECSCICDVGYGGAQCATKVGFPFHTCDLRID 240

Qy        308 GDCFMVSSEADTYYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETR 367
              ||||||| |||||| |:|||| |||||||:||||||||||||||||||||||||||||:
Db        241 GDCFMVSPEADTYYGAKMKCQGKGGVLAQIESQKVQDILAFYLGRLETTNEVTDSDFETK 300

Qy        368 NFWIGLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFN 427
              ||||||||| ||||||| |||||:||||||||||          |||||||:|||||||
Db        301 NFWIGLTYKAAKDSFRWTTGEHQSFTSFAFGQPDN---------QGFGNCVEMQASAAFN 351

Qy        428 WNDQRCKTRNRYICQFAQEHISRWGPG 454
              |||||||||||||||||:| ||| ||
Db        352 WNDQRCKTRNRYICQFAQKHYSRWEPG 378
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RESULT 10
Q8IUW8
ID Q8IUW8 PRELIMINARY; PRT; 301 AA.
AC Q8IUW8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MGC34761.
GN Name=MGC34761;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
DR EMBL; BC039068; AAH39068.1; -.
DR HSSP; P04284; 1CFE.

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DR   GO; GO:0005576; C:extracellular; IEA.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006210; IEGF.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00837; V5TPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS00022; EGF_1; 2.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS50026; EGF_3; 1.
KW   EGF-like domain; Hypothetical protein.
SQ   SEQUENCE   301 AA;  33090 MW;  2F83355A6D1360A0 CRC64;

  Query Match             63.7%;  Score 1611;  DB 2;  Length 301;
  Best Local Similarity   98.6%;  Pred. No. 1.2e-117;
  Matches  286;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         39 MAGALNRKESFLLLSLHNRLRSWVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLAS 98
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db          1 MAGALNRKESFLLLSLHNRLRSWVQPPAADRRRLDWSDSLAQLAQARAALCGIPTPSLAS 60

Qy         99 GLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATS 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GLWRTLQVGWNMQLLPAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATS 120

Qy        159 SQLGCGRHLCSAGQTAIEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAW 218
              ||||||||||||| |||||||||| ||||||||||:|||||||||||||||||||||||
Db        121 SQLGCGRHLCSAGQAAIEAFVCAYSPRGNWEVNGKTIVPYKKGAWCSLCTASVSGCFKAW 180

Qy        219 DHAGGLCEVPRNPCRMSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEEC 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 DHAGGLCEVPRNPCRMSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEEC 240

Qy        279 SCVCDIGYGGAQCATKVHFPFHTCDLRIDGDCFMVSSEADTYYRARMKCQ 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SCVCDIGYGGAQCATKVHFPFHTCDLRIDGDCFMVSSEADTYYRARMKCQ 290


RESULT 11
Q7Z4U9
ID   Q7Z4U9      PRELIMINARY;      PRT;   303 AA.
AC   Q7Z4U9;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Guo J.H., She X.Y., Yu L.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 EGF-like domain.
DR   EMBL; AF428259; AAP97299.1; -.
DR   HSSP; P04284; 1CFE.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006210; IEGF.
DR   Pfam; PF00188; SCP; 1.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS50026; EGF_3; 1.
KW   EGF-like domain; Hypothetical protein.
SQ   SEQUENCE   303 AA;  33059 MW;  3D5D0F2083F4DB18 CRC64;

  Query Match             62.8%;  Score 1587;  DB 2;  Length 303;
  Best Local Similarity   95.3%;  Pred. No. 8.8e-116;
  Matches  284;  Conservative    2;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MLHPETSPGRGHLLAVLLALLGTAWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60

Qy         61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         61 WVQPPAADMRRLDWSDSLAQLAQARAALCGTPTPSLASGLWRTLQVGWNMQLLPAGLASF 120

Qy        121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQAAIEAFVC 180

Qy        181 AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240
              |||| |||||||||:||||||||||||||||||||||||||||||||||||||||||||
Db        181 AYSPRGNWEVNGKTIVPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHG 240

Qy        241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFP 298
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  : ||
Db        241 RLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGEPSAPPRCIFP 298


RESULT 12
Q7Z7I8
ID   Q7Z7I8      PRELIMINARY;      PRT;   303 AA.
AC   Q7Z7I8;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Guo J.H., Zan Q., She X.Y., Li D., Yu L.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 EGF-like domain.
DR   EMBL; AF448856; AAP41924.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   InterPro; IPR000742; EGF_2.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR006210; IEGF.
DR   Pfam; PF00188; SCP; 1.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00181; EGF; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS00022; EGF_1; 1.
DR   PROSITE; PS01186; EGF_2; 2.
DR   PROSITE; PS50026; EGF_3; 1.
KW   EGF-like domain; Hypothetical protein.
SQ   SEQUENCE   303 AA;  33419 MW;  3B73D1D4D06F2891 CRC64;

  Query Match             52.2%;  Score 1321;  DB 2;  Length 303;
  Best Local Similarity   80.3%;  Pred. No. 5.1e-95;
  Matches  245;  Conservative   10;  Mismatches   36;  Indels   14;  Gaps    3;

Qy          1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MLHPETSPGRGHLLAVLLALLGTAWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60

Qy         61 WVQPPAADMRRLDWSDSLAQLAQARAALC------GI-PTPSLASGLWRTLQVGWNMQLL 113
              ||||||| |||||||||   :  : |       |: |    ||||         : :
Db         61 WVQPPAADRRRLDWSDSLANWLKPGSPLWNPNPEPGVRPVAHPASGL-------EHAAVC 113

Qy        114 PAGLASFVEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQT 173
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           |     ::: |||||||||||||||||||||||  |||||||||||||||||||||||||
Db        114 PRAWRPWLKWVSLWFAEGQRYSHAAGECARNAHLTHYTQLVWATSSQLGCGRHLCSAGQA 173

Qy        174 AIEAFVCAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCR 233
              |||||||||||||||||||||:|||||||||||||||| ||||||||||||||||| ||
Db        174 AIEAFVCAYSPGGNWEVNGKTIVPYKKGAWCSLCTASVSCCFKAWDHAGGLCEVPRNSCR 233

Qy        234 MSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCAT 293
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 MSCQNHGRLNISTCHCHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGEPSAPP 293

Qy        294 KVHFP 298
              :  ||
Db        294 RCIFP 298


RESULT 13
Q9BE36
ID   Q9BE36      PRELIMINARY;      PRT;   334 AA.
AC   Q9BE36;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebellum cortex;
RA   Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA   Suzuki Y., Sugano S., Hashimoto K.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB060195; BAB41141.1; -.
DR   HSSP; P04284; 1CFE.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   InterPro; IPR002413; V5_allergen.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00838; V5ALLERGEN.
DR   PRINTS; PR00837; V5TPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00198; SCP; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   334 AA;  35917 MW;  37B37E3D29DC0D19 CRC64;

  Query Match             45.6%;  Score 1154;  DB 2;  Length 334;
  Best Local Similarity   94.2%;  Pred. No. 6.2e-82;
  Matches  212;  Conservative    2;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRS 60
              ||| |||||||||||||| |||||||||||||||||| || ||||||||||||||||||
Db          1 MLHSETSPGRGHLLAVLLAFLGTTWAEVWPPQLQEQAPMARALTRKESFLLLSLHNRLRS 60

Qy         61 WVQPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASF 120
              ||||||||||||||||||||||||||||| ||||||| | |||||||:|||||| |||
Db         61 WVQPPAADMRRLDWSDSLAQLAQARAALCGTPTPSLASAPWHTLQVGWNVQLLPAGSASF 120

Qy        121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVC 180
              |||||||||||||||||||||||||||||||||||||||||||||||| | |||||||
Db        121 VEVVSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSADQAAIEAFVC 180

Qy        181 AYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLC 225
              ||||||||||||||:|||||||||||||||||||||||||||||||
Db        181 AYSPGGNWEVNGKTIVPYKKGAWCSLCTASVSGCFKAWDHAGGLC 225


RESULT 14
Q96HH2
ID   Q96HH2      PRELIMINARY;      PRT;   156 AA.
AC   Q96HH2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   LOC348174 protein (Fragment).
GN   Name=LOC348174;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC008616; AAH08616.1; -.
DR   HSSP; P05452; 1TN3.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   156 AA;  17134 MW;  8A0F06A955C97306 CRC64;

  Query Match             15.7%;  Score 397.5;  DB 2;  Length 156;
  Best Local Similarity   86.9%;  Pred. No. 3.2e-23;
  Matches   73;  Conservative    0;  Mismatches    2;  Indels    9;  Gaps    1;

Qy        372 GLTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQ 431
              |||||||||||||||||||||||||||||  |         ||||||||||||||||||
Db         82 GLTYKTAKDSFRWATGEHQAFTSFAFGQPATH---------GFGNCVELQASAAFNWNDQ 132

Qy        432 RCKTRNRYICQFAQEHISRWGPGS 455
              |||||||||||||||||||||||
Db        133 RCKTRNRYICQFAQEHISRWGPGS 156


RESULT 15
Q6ZVG9
ID   Q6ZVG9      PRELIMINARY;      PRT;   270 AA.
AC   Q6ZVG9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein FLJ42598.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
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RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebellum;
RA   Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA   Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA   Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA   Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA   Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA   Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA   Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK124589; BAC85892.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   InterPro; IPR001283; Allrgn_V5/Tpx1.
DR   Pfam; PF00188; SCP; 1.
DR   PRINTS; PR00837; V5TPXLIKE.
DR   ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR   SMART; SM00198; SCP; 1.
DR   PROSITE; PS01009; CRISP_1; 1.
DR   PROSITE; PS01010; CRISP_2; UNKNOWN_1.
SQ   SEQUENCE   270 AA;  29670 MW;  DCAF708EF0DB19AD CRC64;

  Query Match             11.1%;  Score 280;  DB 2;  Length 270;
  Best Local Similarity   32.3%;  Pred. No. 8.4e-14;
  Matches   75;  Conservative   28;  Mismatches   77;  Indels   52;  Gaps    9;

Qy         13 LLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWVQPPAADMRRL 72
              || :|| |: ||              |: |||  :|  |:: |||  |: | |||:||  :
Db         11 LLPLLLLLVATT-----------GPV-GALTDEEKRLMVELHNLYRAQVSPPASDMLHM 57

Qy         73 DWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFV---------EV 123
               | : ||  |:| |  |          :|     | | :    |   |
Db         58 RWDEELAAFAKAYARQC----------VW-----GHNKERGRRGENLFAITDEGMDVPLA 102

Qy        124 VSLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLC----SAGQTAIEAFV 179
              :  |  | : |: :|  |:    | ||||:||| : ::||| | |       :| ||  |
Db        103 MEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLV 162

Qy        180 CAYSPGGNWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNP 231
              | | | ||  | ||   ||::|  || | :       :     |||   :|
Db        163 CNYEPPGN--VKGKR--PYQEGTPCSQCPS-------GYHCKNSLCEPIGSP 203


Search completed: February 11, 2005, 19:09:10
Job time : 218 secs
```

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GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: February 11, 2005, 18:57:21 ; Search time 167 Seconds
(without alignments)
1053.748 Million cell updates/sec
Title: US-09-943-664-50
Perfect score: 2529
Sequence: 1 MLHPETSPGRGHLLAVLLAL.....RNRYICQFAQEHISRWGPGS 455
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries
Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description

RESULT 1
ID AAY06483 standard; protein; 455 AA.
DE Human tumour-associated protein PRO347.
PN WO9935170-A2.
PD 15-JUL-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 2
ID AAY17828 standard; protein; 455 AA.
DE Human PRO347 protein sequence.
PN WO9928462-A2.
PD 10-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 3
ID AAY93690 standard; protein; 455 AA.
DE Amino acid sequence of novel polypeptide PRO347.
PN WO200037640-A2.
PD 29-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 3; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 4
ID ABU55928 standard; protein; 455 AA.
DE Human secreted/transmembrane protein PRO347.
PN US2002142959-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 6; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 5
ID ABU60238 standard; protein; 455 AA.
DE Human PRO polypeptide #9.
PN US2002132768-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 6; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 6
ID ABU64924 standard; protein; 455 AA.
DE Human secreted/transmembrane protein PRO347.
PN US2002173463-A1.
PD 21-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 6; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 7
ID ABU58358 standard; protein; 455 AA.
DE Novel human secreted protein PRO347.
PN US2002150976-A1.
PD 17-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 6; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 8
ID ABU57244 standard; protein; 455 AA.
DE Human PRO347 protein.
PN US2002142958-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 6; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 9
ID ABU56309 standard; protein; 455 AA.
DE Human secreted/transmembrane protein, PRO347.
PN US2002132981-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 6; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 10
ID ABU60349 standard; protein; 455 AA.
DE Novel human secreted and transmembrane protein PRO347.
PN US2002168715-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 6; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 11
ID ABU11310 standard; protein; 455 AA.
DE Human 347 protein sequence.
PN US2002127643-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 6; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 12
ID ABU67129 standard; protein; 455 AA.
DE Human PRO polypeptide #9.
PN US2002165143-A1.
PD 07-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 6; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 13
ID ADC25806 standard; protein; 455 AA.
DE Human secreted/transmembrane PRO polypeptide #9.
PN US2002142419-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 7; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 14
ID ADC25564 standard; protein; 455 AA.
DE Human secreted/transmembrane PRO polypeptide #9.
PN US2002156004-A1.
PD 24-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 7; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 15
ID ADC25685 standard; protein; 455 AA.
DE Human secreted/transmembrane PRO polypeptide #9.

PN US2003077698-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 7; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 16
ID ADH27470 standard; protein; 455 AA.
DE Human secreted/transmembrane PRO polypeptide #9.
PN US2003083479-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 7; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 17
ID ADE71519 standard; protein; 455 AA.
DE Human secreted/transmembrane PRO polypeptide #9.
PN US2003096742-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 18
ID ADG63462 standard; protein; 455 AA.
DE Human secreted/transmembrane PRO polypeptide #9.
PN US2003211570-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 19
ID ADH43191 standard; protein; 455 AA.
DE Human secreted/transmembrane PRO polypeptide #9.
PN US2003207401-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 20
ID ADN00429 standard; protein; 455 AA.
DE Human secreted/transmembrane PRO polypeptide #9.
PN US2004091972-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 2529; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 5.5e-181;
RESULT 21
ID AAY41266 standard; protein; 446 AA.
DE Human T139 protein.
PN WO9954343-A2.
PD 28-OCT-1999.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 96.8%; Score 2447.5; DB 2; Length 446;
Best Local Similarity 97.1%; Pred. No. 6.8e-175;
RESULT 22
ID AAE06575 standard; protein; 446 AA.
DE Human protein having hydrophobic domain, HP10760.
PN WO200149728-A2.
PD 12-JUL-2001.
PA (PROT-) PROTEGENE INC.
PA (SAGA) SAGAMI CHEM RES CENT.
Query Match 96.8%; Score 2447.5; DB 4; Length 446;
Best Local Similarity 97.1%; Pred. No. 6.8e-175;
RESULT 23
ID AAB64994 standard; protein; 446 AA.
DE Human secreted protein #2.
PN WO200075375-A1.
PD 14-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 96.8%; Score 2447.5; DB 4; Length 446;
Best Local Similarity 97.1%; Pred. No. 6.8e-175;
RESULT 24
ID AAE21077 standard; protein; 446 AA.
DE Human T139 (TANGO-139) protein.
PN US2002028508-A1.
PD 07-MAR-2002.
PA (HOLT/) HOLTZMAN D A.
PA (GOOD/) GOODEARL A D J.
PA (MCCA/) MCCARTHY S A.
Query Match 96.8%; Score 2447.5; DB 5; Length 446;
Best Local Similarity 97.1%; Pred. No. 6.8e-175;
RESULT 25
ID ABW00606 standard; protein; 446 AA.
DE Human T139 protein.
PN US2003104447-A1.
PD 05-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 96.8%; Score 2447.5; DB 7; Length 446;
Best Local Similarity 97.1%; Pred. No. 6.8e-175;
RESULT 26
ID AAM93326 standard; protein; 446 AA.
DE Human polypeptide, SEQ ID NO: 2851.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 95.9%; Score 2426.5; DB 4; Length 446;
Best Local Similarity 96.3%; Pred. No. 2.5e-173;
RESULT 27
ID ADL30818 standard; protein; 446 AA.
DE Human protein encoded by a full length cDNA clone SeqID 2851.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 95.9%; Score 2426.5; DB 8; Length 446;
Best Local Similarity 96.3%; Pred. No. 2.5e-173;
RESULT 28
ID AAY41267 standard; protein; 420 AA.
DE Human T139 mature protein sequence.
PN WO9954343-A2.
PD 28-OCT-1999.
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
Query Match 91.6%; Score 2315.5; DB 2; Length 420;
Best Local Similarity 97.2%; Pred. No. 4.9e-165;
RESULT 29
ID AAE21078 standard; protein; 420 AA.
DE Human T139 (TANGO-139) mature protein.
PN US2002028508-A1.
PD 07-MAR-2002.
PA (HOLT/) HOLTZMAN D A.
PA (GOOD/) GOODEARL A D J.
PA (MCCA/) MCCARTHY S A.
Query Match 91.6%; Score 2315.5; DB 5; Length 420;
Best Local Similarity 97.2%; Pred. No. 4.9e-165;
RESULT 30
ID ABW00607 standard; protein; 420 AA.
DE Human mature T139 protein.
PN US2003104447-A1.
PD 05-JUN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 91.6%; Score 2315.5; DB 7; Length 420;
Best Local Similarity 97.2%; Pred. No. 4.9e-165;
RESULT 31
ID ADE95552 standard; protein; 415 AA.
DE Human NOVX12a protein.
PN WO2003050245-A2.
PD 19-JUN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 88.6%; Score 2241; DB 7; Length 415;
Best Local Similarity 90.3%; Pred. No. 1.8e-159;
RESULT 32
ID ABM85171 standard; protein; 437 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5420.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 88.1%; Score 2227; DB 8; Length 437;
Best Local Similarity 90.1%; Pred. No. 2.2e-158;

RESULT 33
ID ABM85172 standard; protein; 437 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5421.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 88.1%; Score 2227; DB 8; Length 437;
Best Local Similarity 90.1%; Pred. No. 2.2e-158;
RESULT 34
ID ABM84725 standard; protein; 437 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4974.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 87.0%; Score 2201; DB 8; Length 437;
Best Local Similarity 88.8%; Pred. No. 1.9e-156;
RESULT 35
ID ABM84726 standard; protein; 437 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4975.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 87.0%; Score 2201; DB 8; Length 437;
Best Local Similarity 88.8%; Pred. No. 1.9e-156;
RESULT 36
ID ABU11467 standard; protein; 370 AA.
DE Human MDDT polypeptide SEQ ID 414.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 80.1%; Score 2025.5; DB 6; Length 370;
Best Local Similarity 97.0%; Pred. No. 2.2e-143;
RESULT 37
ID ADM80795 standard; protein; 366 AA.
DE Human CADECM-24 protein SEQ ID NO:24.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 78.7%; Score 1989.5; DB 8; Length 366;
Best Local Similarity 80.4%; Pred. No. 1.1e-140;
RESULT 38
ID ABM85170 standard; protein; 366 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5419.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 78.4%; Score 1983.5; DB 8; Length 366;
Best Local Similarity 80.2%; Pred. No. 3.1e-140;
RESULT 39
ID ABG12157 standard; protein; 506 AA.
DE Novel human diagnostic protein #12148.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 77.6%; Score 1961.5; DB 4; Length 506;
Best Local Similarity 73.9%; Pred. No. 2e-138;
RESULT 40
ID ADN42974 standard; protein; 391 AA.
DE Human secreted protein SECP-35.
PN WO2004037987-A2.
PD 06-MAY-2004.
PA (INCY-) INCYTE CORP.
Query Match 72.5%; Score 1834; DB 8; Length 391;
Best Local Similarity 96.8%; Pred. No. 5.2e-129;
RESULT 41
ID ABU11626 standard; protein; 371 AA.
DE Human MDDT polypeptide SEQ ID 573.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 71.5%; Score 1809; DB 6; Length 371;
Best Local Similarity 98.2%; Pred. No. 3.7e-127;
RESULT 42
ID ABG27603 standard; protein; 395 AA.
DE Novel human diagnostic protein #27594.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 68.5%; Score 1732; DB 4; Length 395;
Best Local Similarity 97.8%; Pred. No. 2.3e-121;
RESULT 43
ID ABP96844 standard; protein; 303 AA.
DE Human PREGF protein.
PN CN1366046-A.
PD 28-AUG-2002.
PA (UYFU-) UNIV FUDAN.
Query Match 62.8%; Score 1587; DB 6; Length 303;
Best Local Similarity 95.3%; Pred. No. 1.2e-110;
RESULT 44
ID ABP96845 standard; protein; 276 AA.
DE Human PREGF mature protein.
PN CN1366046-A.
PD 28-AUG-2002.
PA (UYFU-) UNIV FUDAN.
Query Match 57.3%; Score 1450; DB 6; Length 276;
Best Local Similarity 95.2%; Pred. No. 2e-100;
RESULT 45
ID ABG12156 standard; protein; 276 AA.
DE Novel human diagnostic protein #12147.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 45.3%; Score 1145; DB 4; Length 276;
Best Local Similarity 93.9%; Pred. No. 1.4e-77;
RESULT 46
ID AAY70015 standard; protein; 166 AA.
DE Human Protease and associated protein-9 (PPRG-9).
PN WO200009709-A2.
PD 24-FEB-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 34.9%; Score 882; DB 3; Length 166;
Best Local Similarity 99.4%; Pred. No. 4e-58;
RESULT 47
ID ABP96843 standard; peptide; 147 AA.
DE Human PREGF amino acid sequence 44-190.
PN CN1366046-A.
PD 28-AUG-2002.
PA (UYFU-) UNIV FUDAN.
Query Match 30.6%; Score 773; DB 6; Length 147;
Best Local Similarity 98.0%; Pred. No. 5.1e-50;
RESULT 48
ID ABG17023 standard; protein; 493 AA.
DE Novel human diagnostic protein #17014.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 29.1%; Score 735; DB 4; Length 493;
Best Local Similarity 48.6%; Pred. No. 1.4e-46;
RESULT 49
ID AAM23810 standard; protein; 112 AA.
DE Human EST encoded protein SEQ ID NO: 1335.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 23.2%; Score 587; DB 4; Length 112;
Best Local Similarity 99.1%; Pred. No. 3.2e-36;
RESULT 50
ID ABG24318 standard; protein; 1220 AA.
DE Novel human diagnostic protein #24309.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 20.2%; Score 512; DB 4; Length 1220;
Best Local Similarity 56.0%; Pred. No. 2e-29;
RESULT 51
ID ABG12158 standard; protein; 263 AA.

DE Novel human diagnostic protein #12149.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 17.0%; Score 429.5; DB 4; Length 263;
Best Local Similarity 54.6%; Pred. No. 5.3e-24;
RESULT 52
ID ABU92021 standard; protein; 270 AA.
DE Human protein modification and maintenance molecule-1 (PMMM-1).
PN WO2003031939-A2.
PD 17-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.1%; Score 280; DB 6; Length 270;
Best Local Similarity 32.3%; Pred. No. 8.6e-13;
RESULT 53
ID ADQ65201 standard; protein; 270 AA.
DE Novel human protein sequence #174.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 11.1%; Score 280; DB 8; Length 270;
Best Local Similarity 32.3%; Pred. No. 8.6e-13;
RESULT 54
ID ADF79444 standard; protein; 463 AA.
DE Human prostate secretory protein PSP94-binding protein.
PN WO2003093474-A1.
PD 13-NOV-2003.
PA (PROC-) PROCYON BIOPHARMA INC.
Query Match 11.1%; Score 280; DB 7; Length 463;
Best Local Similarity 32.3%; Pred. No. 1.6e-12;
RESULT 55
ID ADH54568 standard; protein; 463 AA.
DE Human leukocyte regulatory factor (LRF)-2 protein.
PN US2003162956-A1.
PD 28-AUG-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 11.1%; Score 280; DB 7; Length 463;
Best Local Similarity 32.3%; Pred. No. 1.6e-12;
RESULT 56
ID ADF79443 standard; protein; 550 AA.
DE Human prostate secretory protein PSP94-binding protein.
PN WO2003093474-A1.
PD 13-NOV-2003.
PA (PROC-) PROCYON BIOPHARMA INC.
Query Match 11.1%; Score 280; DB 7; Length 550;
Best Local Similarity 32.3%; Pred. No. 1.9e-12;
RESULT 57
ID ADF79442 standard; protein; 625 AA.
DE Human prostate secretory protein PSP94-binding protein.
PN WO2003093474-A1.
PD 13-NOV-2003.
PA (PROC-) PROCYON BIOPHARMA INC.
Query Match 11.1%; Score 280; DB 7; Length 625;
Best Local Similarity 32.3%; Pred. No. 2.2e-12;
RESULT 58
ID AAB88408 standard; protein; 463 AA.
DE Human membrane or secretory protein clone PSEC0164.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 11.0%; Score 277; DB 4; Length 463;
Best Local Similarity 32.3%; Pred. No. 2.6e-12;
RESULT 59
ID ADE07929 standard; protein; 506 AA.
DE Novel protein (useful for identifying genetic disorders) #84.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.8%; Score 273; DB 7; Length 506;
Best Local Similarity 32.2%; Pred. No. 5.8e-12;
RESULT 60
ID ADF79437 standard; protein; 506 AA.
DE Human prostate secretory protein PSP94-binding protein.
PN WO2003093474-A1.
PD 13-NOV-2003.
PA (PROC-) PROCYON BIOPHARMA INC.
Query Match 10.8%; Score 273; DB 7; Length 506;
Best Local Similarity 32.2%; Pred. No. 5.8e-12;
RESULT 61
ID ADF79438 standard; protein; 593 AA.
DE Human prostate secretory protein PSP94-binding protein.
PN WO2003093474-A1.
PD 13-NOV-2003.
PA (PROC-) PROCYON BIOPHARMA INC.
Query Match 10.8%; Score 273; DB 7; Length 593;
Best Local Similarity 32.2%; Pred. No. 7e-12;
RESULT 62
ID AAM39716 standard; protein; 266 AA.
DE Human polypeptide SEQ ID NO 2861.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.8%; Score 272; DB 4; Length 266;
Best Local Similarity 31.9%; Pred. No. 3.4e-12;
RESULT 63
ID AAM41502 standard; protein; 347 AA.
DE Human polypeptide SEQ ID NO 6433.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.8%; Score 272; DB 4; Length 347;
Best Local Similarity 31.9%; Pred. No. 4.5e-12;
RESULT 64
ID ADE08995 standard; protein; 347 AA.
DE Novel protein-related contig polypeptide sequence #61.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.8%; Score 272; DB 7; Length 347;
Best Local Similarity 31.9%; Pred. No. 4.5e-12;
RESULT 65
ID ADE10009 standard; protein; 347 AA.
DE Novel protein-related contig polypeptide sequence #597.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.8%; Score 272; DB 7; Length 347;
Best Local Similarity 31.9%; Pred. No. 4.5e-12;
RESULT 66
ID AAY13392 standard; protein; 463 AA.
DE Amino acid sequence of protein PRO328.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 2; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 67
ID AAB01373 standard; protein; 463 AA.
DE Neuron-associated protein.
PN WO200034477-A2.
PD 15-JUN-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 10.8%; Score 272; DB 3; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 68
ID AAY95343 standard; protein; 463 AA.
DE Human PRO328 antitumour protein.
PN WO200037638-A2.
PD 29-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 3; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 69
ID ADC78597 standard; protein; 463 AA.
DE Human PRO328 protein.
PN WO200015796-A2.

PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 3; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 70
ID AAB80260 standard; protein; 463 AA.
DE Human PRO328 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 4; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 71
ID AAU12351 standard; protein; 463 AA.
DE Human PRO328 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 4; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 72
ID AAB53088 standard; protein; 463 AA.
DE Human angiogenesis-associated protein PRO328, SEQ ID NO:132.
PN WO200053753-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 4; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 73
ID ABU71638 standard; protein; 463 AA.
DE Human PRO polypeptide #49.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 74
ID ABO17795 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 75
ID ABU71493 standard; protein; 463 AA.
DE Human PRO polypeptide #49.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 76
ID ABU81049 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 77
ID ABU71939 standard; protein; 463 AA.
DE Human secreted/transmembrane protein PRO328.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 78
ID ABO01822 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 79
ID ABU66749 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 80
ID ABU54395 standard; protein; 463 AA.
DE Human secreted/transmembrane protein PRO328.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 81
ID ABO47410 standard; protein; 463 AA.
DE Human secreted/transmembrane polypeptide PRO328.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 82
ID ABU59830 standard; protein; 463 AA.
DE Novel secreted and transmembrane protein PRO328.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 83
ID ABO25020 standard; protein; 463 AA.
DE Human secreted/transmembrane protein (PRO) #180.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 84
ID ABU64547 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #51.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 85
ID ABU67393 standard; protein; 463 AA.
DE Human secreted protein PRO328.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 86
ID ABO14913 standard; protein; 463 AA.
DE Human secreted / transmembrane polypeptide PRO328.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 87
ID ABU67025 standard; protein; 463 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 360.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 88
ID ABU69670 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 89
ID ABO14852 standard; protein; 463 AA.
DE Human secreted / transmembrane polypeptide PRO328.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 90
ID ADA45879 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 91
ID ADA76310 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 92
ID ADB29490 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 93
ID ADA18960 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 94
ID ADA61583 standard; protein; 463 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 95
ID ADB19368 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 96
ID ADB27909 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 97
ID ADA86388 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 98
ID ADB15952 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 99
ID ADA47738 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 100
ID ADA18346 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 101
ID ABO32804 standard; protein; 463 AA.
DE Human secreted/transmembrane protein PRO328.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 102
ID ADA67533 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 103
ID ADB30540 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 104
ID ADA85836 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 105
ID ADA97048 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;

RESULT 106
ID ADA79352 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 107
ID ADA87491 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 108
ID ADB16693 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 109
ID ABO34864 standard; protein; 463 AA.
DE Human PRO polypeptide #49.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 110
ID ADA16321 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 111
ID ADA91785 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 112
ID ADB14848 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 113
ID ADB18809 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 114
ID ADA94024 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 115
ID ADB19920 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 116
ID ADB13232 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 117
ID ABO43328 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 118
ID ADA74486 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 119
ID ADA42466 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 120
ID ADB24719 standard; protein; 463 AA.
DE Human PRO polypeptide SEQ ID NO 360.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 121
ID ADA82243 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 122
ID ADA75206 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 123
ID ADA85284 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 124
ID ADA84732 standard; protein; 463 AA.

DE Novel human secreted and transmembrane protein PRO328.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 125
ID ABO17542 standard; protein; 463 AA.
DE Human PRO polypeptide #49.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 126
ID ADB29988 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 127
ID ADA80516 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 128
ID ADA75758 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 129
ID ADA46983 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 130
ID ADB25279 standard; protein; 463 AA.
DE Human PRO polypeptide SEQ ID NO 360.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 131
ID ADA93455 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 132
ID ADB26805 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 133
ID ADB31092 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 134
ID ADA61020 standard; protein; 463 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 135
ID ADB24167 standard; protein; 463 AA.
DE Human PRO polypeptide SEQ ID NO 360.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 136
ID ADA96496 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 137
ID ADA81068 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 138
ID ADA95944 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 139
ID ADB26253 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 140
ID ADB21738 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 6; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 141
ID ADA77517 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 142
ID ADB18257 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003077710-A1.

PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 143
ID ADA86940 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 144
ID ADA16745 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 145
ID ADA13174 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 146
ID ADA42042 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 147
ID ADA88043 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 148
ID ADA46431 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 149
ID ADA17389 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 150
ID ADA42892 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 151
ID ADB28461 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 152
ID ADB29013 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 153
ID ADA76965 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 154
ID ADA88595 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 155
ID ADA97600 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 156
ID ADB27357 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 157
ID ADB22290 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 158
ID ABO17603 standard; protein; 463 AA.
DE Human PRO polypeptide #49.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 159
ID ADA66981 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 160
ID ADB22842 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;

RESULT 161
ID ADB23615 standard; protein; 463 AA.
DE Human PRO polypeptide SEQ ID NO 360.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 162
ID ADA92337 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 163
ID ADB15400 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 164
ID ADB38652 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 165
ID ADB38100 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 166
ID ADB66572 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 167
ID ADB89652 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 168
ID ADB90384 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 169
ID ADB77811 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 170
ID ADB39485 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 171
ID ADB74947 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 172
ID ADB47108 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 173
ID ADB86715 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 174
ID ADB77320 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 175
ID ADB34477 standard; protein; 463 AA.
DE Human PRO polypeptide SEQ ID NO 360.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 176
ID ADB35581 standard; protein; 463 AA.
DE Human PRO polypeptide SEQ ID NO 360.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 177
ID ADB33925 standard; protein; 463 AA.
DE Human PRO polypeptide SEQ ID NO 360.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 178
ID ADB35029 standard; protein; 463 AA.
DE Human PRO polypeptide SEQ ID NO 360.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 179
ID ADB36133 standard; protein; 463 AA.

DE Human PRO polypeptide SEQ ID NO 360.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 180
ID ADB46528 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 181
ID ADC28593 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 182
ID ADC39793 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 183
ID ADC40307 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 184
ID ADC19131 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 185
ID ADC34431 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 186
ID ADC29486 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 187
ID ADC29017 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 188
ID ADC40902 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 189
ID ADC19559 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 190
ID ADC34007 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 191
ID ADC13077 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 192
ID ADC50401 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 193
ID ADC71948 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 194
ID ADC59927 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 195
ID ADC52934 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein Seq ID360.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 196
ID ADC57288 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein Seq ID360.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 197
ID ADC60479 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003087367-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 198
ID ADC50954 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 199
ID ADC65481 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 200
ID ADC54579 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein Seq ID360.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 201
ID ADC53540 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein Seq ID360.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 202
ID ADC59063 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein Seq ID360.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 203
ID ADC55941 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein Seq ID360.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 204
ID ADC58511 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein Seq ID360.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 205
ID ADC12529 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 206
ID ADD03185 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 207
ID ADC90177 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 208
ID ADC69596 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 209
ID ADC48485 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 210
ID ADD10014 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 211
ID ADD04589 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 212
ID ADC80545 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 213
ID ADD11052 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 214
ID ADC47933 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 215
ID ADD05084 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 216
ID ADC79993 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 217
ID ADD09462 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 218
ID ADD04090 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 219
ID ADD03666 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 220
ID ADD41175 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 221
ID ADD52314 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 222
ID ADD53054 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 223
ID ADD53606 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 224
ID ADD51762 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 225
ID ADD02561 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 226
ID ADD01995 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 227
ID ADD54177 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 228
ID ADD92494 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 229
ID ADD91390 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 230
ID ADE04004 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 231
ID ADE32301 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 232
ID ADE22233 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 233
ID ADD79457 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;

RESULT 234
ID ADE41993 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 235
ID ADE17810 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 236
ID ADD91942 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 237
ID ADE33405 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 238
ID ADE33957 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 239
ID ADD80009 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 240
ID ADD93046 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 241
ID ADE19466 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 242
ID ADE34918 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 243
ID ADE18914 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 244
ID ADE43110 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 245
ID ADD95899 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 246
ID ADE22785 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 247
ID ADD78903 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 248
ID ADE32853 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 249
ID ADE42545 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 250
ID ADD80561 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 251
ID ADD89589 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 252
ID ADE40873 standard; protein; 463 AA.

DE Human PRO polypeptide #180.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 253
ID ADE04672 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 254
ID ADE92801 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 255
ID ADG21510 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 256
ID ADG23151 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 257
ID ADF97486 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 258
ID ADG80550 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 259
ID ADG79998 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 260
ID ADH59401 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 261
ID ADH55290 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 262
ID ADH55842 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 263
ID ADI38180 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 264
ID ADI64061 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 265
ID ADI65010 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 266
ID ADI63509 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 267
ID ADH81923 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 268
ID ADH81371 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 269
ID ADJ26448 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 270
ID ADM82540 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003087355-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 271
ID ADN15939 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 272
ID ADN16568 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 273
ID ADN15387 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 274
ID ADN14835 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 7; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 275
ID ADC81097 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 276
ID ADE79363 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 277
ID ADD76545 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 278
ID ADD87909 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 279
ID ADD86313 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 280
ID ADE79787 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 281
ID ADE75761 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 282
ID ADE73463 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 283
ID ADE23337 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 284
ID ADE23889 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 285
ID ADE24532 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 286
ID ADD87357 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 287
ID ADE89223 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 288
ID ADE73998 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.

Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 289
ID ADE18362 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 290
ID ADE88671 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 291
ID ADE99552 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 292
ID ADE94691 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 293
ID ADE91102 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 294
ID ADE95243 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 295
ID ADE93353 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 296
ID ADF34934 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 297
ID ADE98671 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 298
ID ADE92249 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 299
ID ADE90550 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 300
ID ADE91697 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 301
ID ADE99098 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 302
ID ADG40568 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 303
ID ADF73962 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 304
ID ADG02276 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 305
ID ADG22062 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 306
ID ADG20132 standard; protein; 463 AA.

DE Human PRO polypeptide #180.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 307
ID ADF98038 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 308
ID ADG24255 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 309
ID ADF98609 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 310
ID ADG03440 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 311
ID ADF99161 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 312
ID ADG16746 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 313
ID ADG05205 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 314
ID ADG19472 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 315
ID ADF73538 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 316
ID ADG13309 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 317
ID ADG08366 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 318
ID ADG15536 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 319
ID ADF96934 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 320
ID ADG06119 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 321
ID ADG23703 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 322
ID ADG03992 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 323
ID ADG24893 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 324
ID ADG07190 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207350-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 325
ID ADG07742 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 326
ID ADG55237 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 327
ID ADG60901 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 328
ID ADG62005 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 329
ID ADG92381 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 330
ID ADG82206 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 331
ID ADG57445 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 332
ID ADG56893 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 333
ID ADG55789 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 334
ID ADG58549 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 335
ID ADG70915 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 336
ID ADG92808 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 337
ID ADG57997 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 338
ID ADG53581 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 339
ID ADG71467 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 340
ID ADG81654 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 341
ID ADH30616 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 342
ID ADH11983 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;

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  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 343
ID   ADG52405 standard; protein; 463 AA.
DE   Novel human secreted and transmembrane protein PRO328.
PN   US2003207414-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 344
ID   ADG54133 standard; protein; 463 AA.
DE   Novel human secreted and transmembrane protein PRO328.
PN   US2003207416-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 345
ID   ADG81102 standard; protein; 463 AA.
DE   Human PRO polypeptide #180.
PN   US2003194793-A1.
PD   16-OCT-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 346
ID   ADG56341 standard; protein; 463 AA.
DE   Novel human secreted and transmembrane protein PRO328.
PN   US2003207366-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 347
ID   ADH12607 standard; protein; 463 AA.
DE   Novel human secreted and transmembrane protein PRO328.
PN   US2003207378-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 348
ID   ADG61453 standard; protein; 463 AA.
DE   Novel human secreted and transmembrane protein PRO328.
PN   US2003207429-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 349
ID   ADH28540 standard; protein; 463 AA.
DE   Human PRO polypeptide #180.
PN   US2003022331-A1.
PD   30-JAN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 350
ID   ADG54685 standard; protein; 463 AA.
DE   Novel human secreted and transmembrane protein PRO328.
PN   US2003207367-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 351
ID   ADG59725 standard; protein; 463 AA.
DE   Novel human secreted and transmembrane protein PRO328.
PN   US2003207369-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 352
ID   ADH20597 standard; protein; 463 AA.
DE   Human secreted/transmembrane protein, #53.
PN   US2004005553-A1.
PD   08-JAN-2004.
PA   (GETH ) GENENTECH INC.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 353
ID   ADH07452 standard; protein; 463 AA.
DE   Human secreted/transmembrane protein, #53.
PN   US2004006211-A1.
PD   08-JAN-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 354
ID   ADH59997 standard; protein; 463 AA.
DE   Human secreted/transmembrane protein, #53.
PN   US2003215904-A1.
PD   20-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 355
ID   ADH07025 standard; protein; 463 AA.
DE   Human secreted/transmembrane protein, #53.
PN   US2004005565-A1.
PD   08-JAN-2004.
PA   (DESN/) DESNOYERS L.
PA   (GODD/) GODDARD A.
PA   (GODO/) GODOWSKI P J.
PA   (GURN/) GURNEY A L.
PA   (MATH/) MATHER J P.
PA   (WILL/) WILLIAMS P M.
PA   (WOOD/) WOOD W I.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 356
ID   ADI81149 standard; protein; 463 AA.
DE   Human PRO polypeptide #180.
PN   US2003207361-A1.
PD   06-NOV-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 357
ID   ADI18767 standard; protein; 463 AA.
DE   Human secreted/transmembrane protein, #53.
PN   US2003152999-A1.
PD   14-AUG-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 358
ID   ADI65487 standard; protein; 463 AA.
DE   Human secreted/transmembrane protein, #53.
PN   US2003148419-A1.
PD   07-AUG-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             10.8%;  Score 272;  DB 8;  Length 463;
  Best Local Similarity   31.9%;  Pred. No. 6.3e-12;
RESULT 359
ID   ADI37746 standard; protein; 463 AA.
DE   Human secreted/transmembrane protein, #53.
PN   US2003096340-A1.
PD   22-MAY-2003.
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PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 360
ID ADG09892 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 361
ID ADH97546 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 362
ID ADI15363 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 363
ID ADG09240 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 364
ID ADI14695 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 365
ID ADH60657 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 366
ID ADI18290 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 367
ID ADJ99714 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 368
ID ADL08907 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 369
ID ADM25248 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 370
ID ADJ63571 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 371
ID ADM29998 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 372
ID ADJ77466 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 373
ID ADJ65588 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 374
ID ADM27724 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 375
ID ADM42448 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 376
ID ADO06320 standard; protein; 463 AA.
DE Human PRO polypeptide #49.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 377

ID ADM28310 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 378
ID ADR11172 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 379
ID ADR18081 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 380
ID ADI95792 standard; protein; 463 AA.
DE Human PRO polypeptide #180.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 381
ID ADI96344 standard; protein; 463 AA.
DE Novel human secreted and transmembrane protein PRO328.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 382
ID ADI65914 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 383
ID ADT03757 standard; protein; 463 AA.
DE Human secreted/transmembrane protein, #53.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 384
ID ADS74720 standard; protein; 463 AA.
DE Human secreted/transmembrane protein #53.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.8%; Score 272; DB 8; Length 463;
Best Local Similarity 31.9%; Pred. No. 6.3e-12;
RESULT 385
ID ADP43676 standard; protein; 225 AA.
DE Human PMMM-33 protein SEQ ID NO:33.
PN WO2004053068-A2.
PD 24-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.7%; Score 271; DB 8; Length 225;
Best Local Similarity 31.9%; Pred. No. 3.3e-12;
RESULT 386
ID ADP07714 standard; protein; 270 AA.
DE Human secreted protein, seq id 197.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.7%; Score 271; DB 8; Length 270;
Best Local Similarity 31.9%; Pred. No. 4e-12;
RESULT 387
ID AAW63115 standard; protein; 270 AA.
DE A human pathogenesis-related protein designated HPRP.
PN WO9829448-A1.
PD 09-JUL-1998.
PA (INCY-) INCYTE PHARM INC.
Query Match 10.6%; Score 267; DB 2; Length 270;
Best Local Similarity 31.5%; Pred. No. 8.1e-12;
RESULT 388
ID AAE10618 standard; protein; 498 AA.
DE Human novel trypsin inhibitor-like protein, NOV-4d.
PN WO200162928-A2.
PD 30-AUG-2001.
PA (CURA-) CURAGEN CORP.
Query Match 10.5%; Score 265; DB 4; Length 498;
Best Local Similarity 26.1%; Pred. No. 2.3e-11;
RESULT 389
ID ADH71198 standard; protein; 498 AA.
DE Human protein of the invention NOV6g SEQ ID NO:94.
PN WO2003102155-A2.
PD 11-DEC-2003.

PA (CURA-) CURAGEN CORP.
Query Match 10.5%; Score 265; DB 8; Length 498;
Best Local Similarity 26.1%; Pred. No. 2.3e-11;
RESULT 390
ID AAB74446 standard; protein; 497 AA.
DE Human protease-inhibitor like protein.
PN WO200121651-A2.
PD 29-MAR-2001.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 10.3%; Score 260.5; DB 4; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 391
ID AAU83619 standard; protein; 497 AA.
DE Human PRO protein, Seq ID No 56.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 5; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 392
ID AAO21721 standard; protein; 497 AA.
DE Human secreted protein SEQ ID No 63.
PN WO200238602-A2.
PD 16-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 10.3%; Score 260.5; DB 5; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 393
ID ABU80766 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 6; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 394
ID ABO33732 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 6; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 395
ID ABU82075 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 6; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 396
ID ABJ72255 standard; protein; 497 AA.
DE Human PRO9783 protein.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 6; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 397
ID ABJ72383 standard; protein; 497 AA.
DE Human PRO9783 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 6; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 398
ID ABO34278 standard; protein; 497 AA.
DE Human secreted/transmembrane polypeptide PRO 9783.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 6; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 399
ID ABJ72085 standard; protein; 497 AA.
DE Human membrane bound receptor/protein PRO9783 amino acid sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 400
ID ADB83546 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 401
ID ADB80652 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 402
ID ADB73193 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 403
ID ADB78275 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 404
ID ADB84923 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 405
ID ADB78029 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 406
ID ADB87095 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 407
ID ADB84677 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;

Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 408
ID ADB83792 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 409
ID ADB72947 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 410
ID ADC36785 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 411
ID ADC21775 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 412
ID ADC49806 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 413
ID ADC49005 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 414
ID ADC49522 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 415
ID ADC47383 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 416
ID ADC47128 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 417
ID ADC78003 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 418
ID ADD06238 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 419
ID ADC77757 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 420
ID ADD50720 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 421
ID ADD50966 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 422
ID ADD50447 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 423
ID ADD50201 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 424
ID ADD51212 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 7; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 425
ID ADC48759 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 426

ID ADE20930 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 427
ID ADE05774 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 428
ID ADD75003 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 429
ID ADD75749 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 430
ID ADD84981 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 431
ID ADD86807 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 432
ID ADE20684 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 433
ID ADE38981 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 434
ID ADE05528 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 435
ID ADD73513 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 436
ID ADD78353 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 437
ID ADE21176 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 438
ID ADD77291 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 439
ID ADE20438 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 440
ID ADD75503 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 441
ID ADD74019 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 442
ID ADD74265 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 443
ID ADD75995 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 444
ID ADD85487 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.

PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 445
ID ADE05036 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 446
ID ADD75249 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 447
ID ADD76793 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 448
ID ADD86561 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 449
ID ADD78029 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 450
ID ADD77537 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 451
ID ADD77783 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 452
ID ADD85241 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 453
ID ADD73773 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 454
ID ADD74511 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 455
ID ADD77039 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 456
ID ADD85733 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 457
ID ADE05282 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 458
ID ADD74757 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 459
ID ADG05569 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 460
ID ADG27123 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 461
ID ADG11186 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 462
ID ADG11965 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003096963-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 463
ID ADF94522 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 464
ID ADG06618 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 465
ID ADH38962 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 466
ID ADH71204 standard; protein; 497 AA.
DE Human protein of the invention NOV6j SEQ ID NO:100.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 467
ID ADG34052 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 468
ID ADI33522 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 469
ID ADH69616 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 470
ID ADI29777 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 471
ID ADM27174 standard; protein; 497 AA.
DE Novel human secreted and transmembrane protein PRO9783.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 472
ID ADK66532 standard; protein; 497 AA.
DE Human PRO polypeptide #28.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.3%; Score 260.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 4.9e-11;
RESULT 473
ID AAE10616 standard; protein; 497 AA.
DE Human novel trypsin inhibitor-like protein, NOV-4b.
PN WO200162928-A2.
PD 30-AUG-2001.
PA (CURA-) CURAGEN CORP.
Query Match 10.3%; Score 259.5; DB 4; Length 497;
Best Local Similarity 26.1%; Pred. No. 5.9e-11;
RESULT 474
ID ADH71196 standard; protein; 497 AA.
DE Human protein of the invention NOV6f SEQ ID NO:92.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.3%; Score 259.5; DB 8; Length 497;
Best Local Similarity 26.1%; Pred. No. 5.9e-11;
RESULT 475
ID AAE02211 standard; protein; 258 AA.
DE Human full-length 36P1G3/SGP28 protein.
PN WO200131343-A2.
PD 03-MAY-2001.
PA (UROG-) UROGENESYS INC.
Query Match 10.2%; Score 259; DB 4; Length 258;
Best Local Similarity 27.1%; Pred. No. 3e-11;
RESULT 476
ID ADH71206 standard; protein; 497 AA.
DE Human protein of the invention NOV6k SEQ ID NO:102.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.2%; Score 258.5; DB 8; Length 497;
Best Local Similarity 25.5%; Pred. No. 7e-11;
RESULT 477
ID ABU53236 standard; protein; 450 AA.
DE Human testes-derived protein from DKFZphtes3_4b4.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 10.2%; Score 257.5; DB 4; Length 450;
Best Local Similarity 25.8%; Pred. No. 7.4e-11;
RESULT 478
ID ABB80592 standard; protein; 497 AA.
DE Human sbg1002620TIa protein #2.
PN WO200222802-A1.
PD 21-MAR-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 10.2%; Score 257.5; DB 5; Length 497;
Best Local Similarity 25.8%; Pred. No. 8.3e-11;
RESULT 479
ID AAE23977 standard; protein; 497 AA.
DE Human LP095 secreted protein.
PN WO200226801-A2.
PD 04-APR-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 10.2%; Score 257.5; DB 5; Length 497;
Best Local Similarity 25.8%; Pred. No. 8.3e-11;
RESULT 480
ID ADE59057 standard; protein; 497 AA.
DE Human Protein NP_113664, SEQ ID NO 4948.
PN WO2003016475-A2.
PD 27-FEB-2003.

PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.2%; Score 257.5; DB 7; Length 497;
Best Local Similarity 25.8%; Pred. No. 8.3e-11;
RESULT 481
ID ADE59061 standard; protein; 497 AA.
DE Human Protein NP_113664, SEQ ID NO 4952.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 10.2%; Score 257.5; DB 7; Length 497;
Best Local Similarity 25.8%; Pred. No. 8.3e-11;
RESULT 482
ID ADP25254 standard; protein; 497 AA.
DE PRO polypeptide SEQ ID NO:2432.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 10.2%; Score 257.5; DB 8; Length 497;
Best Local Similarity 25.8%; Pred. No. 8.3e-11;
RESULT 483
ID AAB93979 standard; protein; 371 AA.
DE Human protein sequence SEQ ID NO:14059.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 10.2%; Score 257; DB 4; Length 371;
Best Local Similarity 28.8%; Pred. No. 6.5e-11;
RESULT 484
ID ADH71202 standard; protein; 475 AA.
DE Human protein of the invention NOV6i SEQ ID NO:98.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.1%; Score 256.5; DB 8; Length 475;
Best Local Similarity 25.8%; Pred. No. 9.3e-11;
RESULT 485
ID AAE10617 standard; protein; 477 AA.
DE Human novel trypsin inhibitor-like protein, NOV-4c.
PN WO200162928-A2.
PD 30-AUG-2001.
PA (CURA-) CURAGEN CORP.
Query Match 10.1%; Score 256.5; DB 4; Length 477;
Best Local Similarity 25.8%; Pred. No. 9.4e-11;
RESULT 486
ID ADH71194 standard; protein; 477 AA.
DE Human protein of the invention NOV6e SEQ ID NO:90.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.1%; Score 256.5; DB 8; Length 477;
Best Local Similarity 25.8%; Pred. No. 9.4e-11;
RESULT 487
ID ADE08679 standard; protein; 781 AA.
DE Novel protein (useful for identifying genetic disorders) #834.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.1%; Score 256; DB 7; Length 781;
Best Local Similarity 32.6%; Pred. No. 1.8e-10;
RESULT 488
ID AAR79914 standard; protein; 198 AA.
DE Trypsin inhibitory protein, isolated from human T98G cells.
PN JP07242700-A.
PD 19-SEP-1995.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 10.1%; Score 254.5; DB 2; Length 198;
Best Local Similarity 29.2%; Pred. No. 4.9e-11;
RESULT 489
ID AAE18962 standard; protein; 255 AA.
DE Mouse testes-specific, vespid and pathogenic protein (RTVP).
PN WO200206344-A2.
PD 24-JAN-2002.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 10.1%; Score 254.5; DB 5; Length 255;
Best Local Similarity 31.0%; Pred. No. 6.5e-11;
RESULT 490
ID ABG61801 standard; protein; 258 AA.
DE Prostate cancer-associated protein #2.
PN WO200230268-A2.
PD 18-APR-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.1%; Score 254.5; DB 5; Length 258;
Best Local Similarity 29.2%; Pred. No. 6.6e-11;
RESULT 491
ID ABG61802 standard; protein; 258 AA.
DE Prostate cancer-associated protein #3.
PN WO200230268-A2.
PD 18-APR-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.1%; Score 254.5; DB 5; Length 258;
Best Local Similarity 29.2%; Pred. No. 6.6e-11;
RESULT 492
ID ABJ05597 standard; protein; 258 AA.
DE Breast cancer-associated protein 62.
PN WO200259377-A2.
PD 01-AUG-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 10.1%; Score 254.5; DB 5; Length 258;
Best Local Similarity 29.2%; Pred. No. 6.6e-11;
RESULT 493
ID ADR14401 standard; protein; 258 AA.
DE Human NF-kappaB pathway-associated protein SeqID402.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 10.1%; Score 254.5; DB 8; Length 258;
Best Local Similarity 29.2%; Pred. No. 6.6e-11;
RESULT 494
ID ABO00573 standard; protein; 253 AA.
DE Novel human polypeptide #160.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 253; DB 6; Length 253;
Best Local Similarity 34.7%; Pred. No. 8.4e-11;
RESULT 495
ID ABU52370 standard; protein; 253 AA.
DE Human GPCR related protein NOV24a.
PN WO200279398-A2.
PD 10-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 10.0%; Score 253; DB 6; Length 253;
Best Local Similarity 34.7%; Pred. No. 8.4e-11;
RESULT 496
ID ADL24075 standard; protein; 253 AA.
DE Human NOVX polypeptide #60.
PN US2004002120-A1.
PD 01-JAN-2004.
PA (KEKU/) KEKUDA R.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (GORM/) GORMAN L.
PA (MALY/) MALYANKAR U M.
PA (BOLD/) BOLDOG F L.
PA (GUOX/) GUO X.
PA (SHEN/) SHENOY S G.
PA (PADI/) PADIGARU M.
PA (TAUP/) TAUPIER R J.
PA (MILL/) MILLER C E.

PA (CASM/) CASMAN S J.
PA (PENA/) PENA C E A.
PA (GANG/) GANGOLLI E A.
PA (GUSE/) GUSEV V Y.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (GERL/) GERLACH V.
PA (POCH/) POCHART P F.
PA (FERN/) FERNANDES E R.
PA (SHIM/) SHIMKETS R A.
PA (RAST/) RASTELLI L.
PA (SPAD/) SPADERNA S K.
PA (LARO/) LAROCHELLE W J.
PA (ZHON/) ZHONG M.
PA (KHRA/) KHRAMTSOV N V.
PA (VOSS/) VOSS E Z.
PA (HERR/) HERRMANN J L.
Query Match 10.0%; Score 253; DB 8; Length 253;
Best Local Similarity 34.7%; Pred. No. 8.4e-11;
RESULT 497
ID AAG79301 standard; protein; 258 AA.
DE Protein encoded by chicken GW159 cDNA.
PN WO200059938-A1.
PD 12-OCT-2000.
PA (GEMY) GENETICS INST INC.
Query Match 10.0%; Score 252.5; DB 3; Length 258;
Best Local Similarity 28.8%; Pred. No. 9.3e-11;
RESULT 498
ID AAM24000 standard; protein; 245 AA.
DE Human EST encoded protein SEQ ID NO: 1525.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 252; DB 4; Length 245;
Best Local Similarity 27.1%; Pred. No. 9.6e-11;
RESULT 499
ID AAM23992 standard; protein; 245 AA.
DE Human EST encoded protein SEQ ID NO: 1517.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.0%; Score 252; DB 4; Length 245;
Best Local Similarity 27.1%; Pred. No. 9.6e-11;
RESULT 500
ID ADB75539 standard; protein; 245 AA.
DE Prostate cancer marker protein.
PN WO2003009814-A2.
PD 06-FEB-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.0%; Score 252; DB 7; Length 245;
Best Local Similarity 27.1%; Pred. No. 9.6e-11;
RESULT 501
ID ADE94309 standard; protein; 245 AA.
DE Human cysteine-rich secretory protein 3 SEQ ID NO:6.
PN WO2003100025-A2.
PD 04-DEC-2003.
PA (MINU) UNIV MINNESOTA.
PA (HAMI/) HAMILTON D W.
PA (ROBE/) ROBERTS K P.
PA (ENSR/) ENSRUD K M.
Query Match 10.0%; Score 252; DB 8; Length 245;
Best Local Similarity 27.1%; Pred. No. 9.6e-11;
RESULT 502
ID ADR66069 standard; protein; 250 AA.
DE Human prostatic carcinoma derived protein SEQ ID 265 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 10.0%; Score 252; DB 8; Length 250;
Best Local Similarity 27.1%; Pred. No. 9.8e-11;
RESULT 503
ID ADR66411 standard; protein; 250 AA.
DE Human prostatic carcinoma derived protein SEQ ID 265 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Query Match 10.0%; Score 252; DB 8; Length 250;
Best Local Similarity 27.1%; Pred. No. 9.8e-11;
RESULT 504
ID ABR39981 standard; protein; 497 AA.
DE Human late gestation lung 1 (LGL1) polypeptide.
PN WO2003020766-A1.
PD 13-MAR-2003.
PA (UYMC-) UNIV MCGILL.
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
Query Match 9.9%; Score 251; DB 6; Length 497;
Best Local Similarity 28.2%; Pred. No. 2.5e-10;
RESULT 505
ID ABR39980 standard; protein; 497 AA.
DE Rat late gestation lung 1 (LGL1) polypeptide.
PN WO2003020766-A1.
PD 13-MAR-2003.
PA (UYMC-) UNIV MCGILL.
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
Query Match 9.9%; Score 251; DB 6; Length 497;
Best Local Similarity 28.2%; Pred. No. 2.5e-10;
RESULT 506
ID AAM24028 standard; protein; 241 AA.
DE Rat EST encoded protein SEQ ID NO: 1553.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.8%; Score 249; DB 4; Length 241;
Best Local Similarity 34.0%; Pred. No. 1.6e-10;
RESULT 507
ID AAU12302 standard; protein; 242 AA.
DE Human PRO7434 polypeptide sequence.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 4; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 508
ID ABO17746 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 509
ID ABU81000 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 510
ID ABU66700 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 511
ID ABU59781 standard; protein; 242 AA.

DE Novel secreted and transmembrane protein PRO7434.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 512
ID ABO24971 standard; protein; 242 AA.
DE Human secreted/transmembrane protein (PRO) #131.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 513
ID ABU66976 standard; protein; 242 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 262.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 514
ID ADA45781 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 515
ID ADA76212 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 516
ID ADA18862 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 517
ID ADA61485 standard; protein; 242 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 518
ID ADB19270 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 519
ID ADB27811 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 520
ID ADA86290 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 521
ID ADB15854 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 522
ID ADA47640 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 523
ID ADA67435 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 524
ID ADB30442 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 525
ID ADA85738 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 526
ID ADA96950 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 527
ID ADA79254 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 528
ID ADA87393 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 529
ID ADB16595 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003087349-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 530
ID ADA91687 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 531
ID ADB14750 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 532
ID ADB18711 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 533
ID ADA93926 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 534
ID ADB19822 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 535
ID ADB13134 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 536
ID ABO43279 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 537
ID ADA74388 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 538
ID ADB24621 standard; protein; 242 AA.
DE Human PRO polypeptide SEQ ID NO 262.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 539
ID ADA82145 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 540
ID ADA75108 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 541
ID ADA85186 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 542
ID ADA84634 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 543
ID ADB29890 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 544
ID ADA80418 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 545
ID ADA75660 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 546
ID ADA46885 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 547
ID ADB25181 standard; protein; 242 AA.
DE Human PRO polypeptide SEQ ID NO 262.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 548
ID ADA93357 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 549
ID ADB26707 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 550
ID ADB30994 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 551
ID ADA60922 standard; protein; 242 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 552
ID ADB24069 standard; protein; 242 AA.
DE Human PRO polypeptide SEQ ID NO 262.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 553
ID ADA96398 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 554
ID ADA80970 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 555
ID ADA95846 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 556
ID ADB26155 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 557
ID ADB21640 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 6; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 558
ID ADA77419 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 559
ID ADB18159 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 560
ID ADA86842 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 561
ID ADA87945 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 562
ID ADA46333 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 563
ID ADB28363 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 564
ID ADB28915 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 565
ID ADA76867 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 566
ID ADA88497 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 567
ID ADA97502 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 568
ID ADB27259 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 569
ID ADB22192 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 570
ID ADA66883 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 571
ID ADB22744 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 572
ID ADB23517 standard; protein; 242 AA.
DE Human PRO polypeptide SEQ ID NO 262.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 573
ID ADA92239 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 574
ID ADB15302 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 575
ID ADB38554 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 576
ID ADB38002 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 577
ID ADB66474 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 578
ID ADB89554 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 579
ID ADB90286 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 580
ID ADB39387 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 581
ID ADB47010 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 582
ID ADB86617 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 583
ID ADB77222 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 584
ID ADB34379 standard; protein; 242 AA.
DE Human PRO polypeptide SEQ ID NO 262.
PN US2003077717-A1.

PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 585
ID ADB35483 standard; protein; 242 AA.
DE Human PRO polypeptide SEQ ID NO 262.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 586
ID ADB33827 standard; protein; 242 AA.
DE Human PRO polypeptide SEQ ID NO 262.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 587
ID ADB34931 standard; protein; 242 AA.
DE Human PRO polypeptide SEQ ID NO 262.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 588
ID ADB36035 standard; protein; 242 AA.
DE Human PRO polypeptide SEQ ID NO 262.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 589
ID ADB46430 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 590
ID ADC50303 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 591
ID ADC71850 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 592
ID ADC59829 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 593
ID ADC52836 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein Seq ID262.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 594
ID ADC57190 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein Seq ID262.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 595
ID ADC60381 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 596
ID ADC50856 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 597
ID ADC65383 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 598
ID ADC54481 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein Seq ID262.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 599
ID ADC53442 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein Seq ID262.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 600
ID ADC58965 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein Seq ID262.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 601
ID ADC55843 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein Seq ID262.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 602
ID ADC58413 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein Seq ID262.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 603
ID ADD03087 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 604
ID ADC90079 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 605
ID ADC69498 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 606
ID ADC48387 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 607
ID ADD09916 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 608
ID ADD04491 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 609
ID ADC80447 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 610
ID ADD10954 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 611
ID ADC47835 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 612
ID ADC79895 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 613
ID ADD09364 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 614
ID ADD41077 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 615
ID ADD52216 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 616
ID ADD52956 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 617
ID ADD53508 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 618
ID ADD51664 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 619
ID ADD02463 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 620
ID ADD01897 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 621
ID ADD54079 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 622
ID ADD92396 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 623
ID ADD91292 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 624
ID ADE03906 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 625
ID ADE32203 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 626
ID ADE22135 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 627
ID ADD79359 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 628
ID ADE41895 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 629
ID ADE17712 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 630
ID ADD91844 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 631
ID ADE33307 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 632
ID ADE33859 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 633
ID ADD79911 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 634
ID ADD92948 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 635
ID ADE19368 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 636
ID ADE18816 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 637
ID ADE43012 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 638
ID ADD95801 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 639
ID ADE22687 standard; protein; 242 AA.

DE Human PRO polypeptide #131.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 640
ID ADD78805 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 641
ID ADE32755 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 642
ID ADE42447 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 643
ID ADD80463 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 644
ID ADD89491 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 645
ID ADE40775 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 646
ID ADE04574 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 647
ID ADE92703 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 648
ID ADG21412 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 649
ID ADG23053 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 650
ID ADF97388 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 651
ID ADG80452 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 652
ID ADG79900 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 653
ID ADH55192 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 654
ID ADH55744 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 655
ID ADI63963 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 656
ID ADI64912 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 657
ID ADH81825 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207388-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 658
ID ADH81273 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 659
ID ADM82442 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 660
ID ADN15841 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 661
ID ADN16470 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 662
ID ADN15289 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 663
ID ADN14737 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 664
ID ADI63411 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 7; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 665
ID ADC80999 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 666
ID ADD76447 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 667
ID ADD87811 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 668
ID ADD86215 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 669
ID ADE75663 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 670
ID ADE23239 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 671
ID ADE23791 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 672
ID ADE24434 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 673
ID ADD87259 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 674
ID ADE89125 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 675
ID ADE18264 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 676
ID ADE88573 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 677
ID ADE94593 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 678
ID ADE91004 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 679
ID ADE95145 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 680
ID ADE93255 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 681
ID ADF34836 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 682
ID ADE92151 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 683
ID ADE90452 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 684
ID ADE91599 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 685
ID ADG02178 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 686
ID ADG21964 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 687
ID ADG20034 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 688
ID ADF97940 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 689
ID ADG24157 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 690
ID ADF98511 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 691
ID ADG03342 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 692
ID ADF99063 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 693
ID ADG16648 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;

RESULT 694
ID ADG05107 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 695
ID ADG19374 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 696
ID ADG13211 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 697
ID ADG08268 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 698
ID ADG15438 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 699
ID ADF96836 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 700
ID ADG06021 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 701
ID ADG23605 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 702
ID ADG03894 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 703
ID ADG24795 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 704
ID ADG07092 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 705
ID ADG07644 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 706
ID ADG55139 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 707
ID ADG60803 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 708
ID ADG61907 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 709
ID ADG82108 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 710
ID ADG57347 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 711
ID ADG56795 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 712
ID ADG55691 standard; protein; 242 AA.

DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 713
ID ADG58451 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 714
ID ADG70817 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 715
ID ADG57899 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 716
ID ADG53483 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 717
ID ADG71369 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 718
ID ADG81556 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207805-A1.
PD 06-NOV-2003.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 719
ID ADH30518 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 720
ID ADH11885 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 721
ID ADG52307 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 722
ID ADG54035 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 723
ID ADG81004 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 724
ID ADG56243 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 725
ID ADH12509 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 726
ID ADG61355 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 727
ID ADH28442 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 728
ID ADG54587 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 729
ID ADG59627 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 730
ID ADI81051 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003207361-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 731
ID ADG09794 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 732
ID ADI15265 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 733
ID ADG09142 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 734
ID ADI14597 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 735
ID ADI18192 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 736
ID ADJ63473 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 737
ID ADJ77368 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 738
ID ADJ65490 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 739
ID ADM27626 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 740
ID ADM42350 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 741
ID ADM28212 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 742
ID ADI95694 standard; protein; 242 AA.
DE Human PRO polypeptide #131.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 743
ID ADI96246 standard; protein; 242 AA.
DE Novel human secreted and transmembrane protein PRO7434.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.8%; Score 249; DB 8; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.6e-10;
RESULT 744
ID ABB80591 standard; protein; 252 AA.
DE Human sbg1002620TIa protein #1.
PN WO200222802-A1.
PD 21-MAR-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 9.8%; Score 249; DB 5; Length 252;
Best Local Similarity 34.0%; Pred. No. 1.7e-10;
RESULT 745
ID AAR79915 standard; protein; 188 AA.
DE Human trypsin inhibitory protein, residues 11-198.
PN JP07242700-A.
PD 19-SEP-1995.
PA (MOCH) MOCHIDA PHARM CO LTD.
Query Match 9.8%; Score 248.5; DB 2; Length 188;
Best Local Similarity 30.3%; Pred. No. 1.3e-10;
RESULT 746
ID AAB47998 standard; protein; 242 AA.
DE Apple crisp protein.
PN WO200059938-A1.
PD 12-OCT-2000.
PA (GEMY) GENETICS INST INC.
Query Match 9.8%; Score 248; DB 3; Length 242;
Best Local Similarity 34.1%; Pred. No. 1.9e-10;
RESULT 747
ID ABB80593 standard; protein; 438 AA.
DE Human sbg1002620TIb protein.
PN WO200222802-A1.
PD 21-MAR-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 9.7%; Score 246.5; DB 5; Length 438;
Best Local Similarity 25.8%; Pred. No. 4.8e-10;
RESULT 748
ID ADL35345 standard; protein; 495 AA.
DE Murine secreted extracellular matrix 33145 protein.

PN JP2004008021-A.
PD 15-JAN-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (DANA-) DANAFOMU KK.
Query Match 9.7%; Score 246; DB 8; Length 495;
Best Local Similarity 28.0%; Pred. No. 6e-10;
RESULT 749
ID ADA57226 standard; protein; 233 AA.
DE Human secreted protein #509.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 245; DB 6; Length 233;
Best Local Similarity 34.2%; Pred. No. 3e-10;
RESULT 750
ID ADA41107 standard; protein; 233 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 245; DB 6; Length 233;
Best Local Similarity 34.2%; Pred. No. 3e-10;
RESULT 751
ID ADC74330 standard; protein; 233 AA.
DE Human secreted protein - SEQ ID 963.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.7%; Score 245; DB 7; Length 233;
Best Local Similarity 34.2%; Pred. No. 3e-10;
RESULT 752
ID ADE86030 standard; protein; 233 AA.
DE Human sperm polypeptide CRISPY.
PN WO2003087151-A1.
PD 23-OCT-2003.
PA (MONU) UNIV MONASH.
Query Match 9.7%; Score 245; DB 7; Length 233;
Best Local Similarity 34.2%; Pred. No. 3e-10;
RESULT 753
ID AAU08687 standard; protein; 300 AA.
DE Human FCTR7 polypeptide sequence.
PN WO200166747-A2.
PD 13-SEP-2001.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 241; DB 4; Length 300;
Best Local Similarity 34.7%; Pred. No. 8.1e-10;
RESULT 754
ID ABU53237 standard; protein; 185 AA.
DE Human testes-derived DKFZphtes3_4b4 homologue #1.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 9.5%; Score 240; DB 4; Length 185;
Best Local Similarity 34.0%; Pred. No. 5.5e-10;
RESULT 755
ID ADE59059 standard; protein; 188 AA.
DE Rat Protein AAD16986, SEQ ID NO 4950.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 9.5%; Score 240; DB 7; Length 188;
Best Local Similarity 34.0%; Pred. No. 5.6e-10;
RESULT 756
ID ADE59055 standard; protein; 188 AA.
DE Rat Protein AAD16986, SEQ ID NO 4946.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 9.5%; Score 240; DB 7; Length 188;
Best Local Similarity 34.0%; Pred. No. 5.6e-10;

RESULT 757
ID ADF74426 standard; protein; 261 AA.
DE Human differentially methylated in cancer (DMC-1) protein.
PN WO2003093507-A1.
PD 13-NOV-2003.
PA (UYBR-) UNIV BRISTOL.
PA (UMOR) UNIV MISSOURI.
Query Match 9.5%; Score 239; DB 7; Length 261;
Best Local Similarity 33.5%; Pred. No. 9.7e-10;
RESULT 758
ID AAB41816 standard; protein; 431 AA.
DE Human ORFX ORF1580 polypeptide sequence SEQ ID NO:3160.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 237.5; DB 3; Length 431;
Best Local Similarity 25.3%; Pred. No. 2.2e-09;
RESULT 759
ID AAE10619 standard; protein; 501 AA.
DE Human novel trypsin inhibitor-like protein, NOV-4e.
PN WO200162928-A2.
PD 30-AUG-2001.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 237.5; DB 4; Length 501;
Best Local Similarity 25.8%; Pred. No. 2.6e-09;
RESULT 760
ID ADH71200 standard; protein; 501 AA.
DE Human protein of the invention NOV6h SEQ ID NO:96.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 237.5; DB 8; Length 501;
Best Local Similarity 25.8%; Pred. No. 2.6e-09;
RESULT 761
ID ABG19776 standard; protein; 348 AA.
DE Novel human diagnostic protein #19767.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.4%; Score 236.5; DB 4; Length 348;
Best Local Similarity 30.9%; Pred. No. 2.1e-09;
RESULT 762
ID ADO31202 standard; protein; 1268 AA.
DE Mouse neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 9.3%; Score 236; DB 8; Length 1268;
Best Local Similarity 25.3%; Pred. No. 9.7e-09;
RESULT 763
ID AAY41738 standard; protein; 500 AA.
DE Human PRO541 protein sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 2; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 764
ID AAB44294 standard; protein; 500 AA.
DE Human PRO541 (UNQ342) protein sequence SEQ ID NO:363.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 3; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 765
ID AAB47999 standard; protein; 500 AA.
DE Cocoa crisp protein.
PN WO200059938-A1.
PD 12-OCT-2000.
PA (GEMY) GENETICS INST INC.
Query Match 9.3%; Score 235.5; DB 3; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;

RESULT 766
ID AAU29058 standard; protein; 500 AA.
DE Human PRO polypeptide sequence #35.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 4; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 767
ID ABG90983 standard; protein; 500 AA.
DE Breast specifc polypeptide #12.
PN WO200264741-A2.
PD 22-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 9.3%; Score 235.5; DB 5; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 768
ID ABU58434 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 769
ID ABU87982 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 770
ID ABU84297 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 771
ID ABR66171 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 772
ID ABR65561 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 773
ID ABU99501 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 774
ID ABU82740 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 775
ID ABU89861 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 776
ID ABR68110 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 777
ID ABU96163 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 778
ID ABU92594 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 779
ID ABO08671 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 780
ID ABO02723 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 781
ID ABR74877 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 782
ID ABR94639 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 783
ID ABO25240 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 784
ID ABU85612 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 785
ID ABU98772 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 786
ID ABU97987 standard; protein; 500 AA.

DE Novel human secreted and transmembrane protein PRO541.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 787
ID ABU91693 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 788
ID ABU72246 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 789
ID ABU89386 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 790
ID ABU86227 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 791
ID ABU67440 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 792
ID ABU80468 standard; protein; 500 AA.
DE Human PRO protein #35.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 793
ID ABR99386 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 794
ID ABR98776 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 795
ID ABO16299 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 796
ID ABR92199 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 797
ID ABO18840 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 798
ID ABR78261 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 799
ID ABU84997 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 800
ID ABO00136 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 801
ID ABO11468 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 802
ID ABO02113 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 803
ID ABU88687 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 804
ID ABU83382 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 805
ID ABO06183 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 806
ID ABR59219 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.

PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 807
ID ABO09281 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 808
ID ABO19145 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 809
ID ABO11163 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 810
ID ABR66781 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 811
ID ABO15994 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 812
ID ABO13700 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 813
ID ABU84926 standard; protein; 500 AA.
DE Human secreted and transmembrane PRO polypeptide #2.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 814
ID ABU65603 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, SEQ ID 70.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 815
ID ABO07451 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 816
ID ABO03638 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 817
ID ABR67086 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 818
ID ABO15689 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 819
ID ABU55970 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 820
ID ABU61124 standard; protein; 500 AA.
DE Human PRO541 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 821
ID ABU65298 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 822
ID ABU95243 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 823
ID ABU71146 standard; protein; 500 AA.
DE Human PRO541 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 824
ID ABO07756 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 825
ID ABR69997 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 826
ID ABR69330 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003036132-A1.

PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 827
ID ABO01471 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 828
ID ABU81273 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 829
ID ABR60070 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 830
ID ABR67805 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 831
ID ABR65193 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 832
ID ABR68415 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 833
ID ABR71827 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 834
ID ABU85307 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 835
ID ABU88997 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 836
ID ABU83077 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 837
ID ABU94933 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 838
ID ABU90481 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 839
ID ABU83992 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 840
ID ABU93643 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 841
ID ABR64888 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 842
ID ABR68720 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 843
ID ABO06536 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 844
ID ABR99081 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 845
ID ABU56965 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 846
ID ABU85917 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;

RESULT 847
ID ABU82204 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 848
ID ABU87215 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 849
ID ABU83687 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 850
ID ABO08061 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 851
ID ABU81772 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 852
ID ABU65936 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 853
ID ABR59765 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 854
ID ABU93953 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 855
ID ABU80393 standard; protein; 500 AA.
DE Human secreted/transmembrane protein PRO541.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 856
ID ABU99806 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 857
ID ABR66476 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 858
ID ABR90894 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 859
ID ABU94321 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 860
ID ABU79203 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 861
ID ABU86532 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 862
ID ABU86837 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 863
ID ABU94626 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 864
ID ABO04553 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 865
ID ABR70302 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 866
ID ABU98467 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 867
ID ABR65866 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003036165-A1.

PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 868
ID ABR64583 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 869
ID ABU79508 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 870
ID ABU92899 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 871
ID ABU95858 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 872
ID ABU91078 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 873
ID ABU90171 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 874
ID ABO09586 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 875
ID ABO10858 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 876
ID ABR70912 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 877
ID ABU87520 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 878
ID ABU91388 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 879
ID ABU84602 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 880
ID ABR69692 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 881
ID ABU80069 standard; protein; 500 AA.
DE Human PRO protein #35.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 882
ID ABU93338 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 883
ID ABO09891 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 884
ID ABO08976 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 885
ID ABU10544 standard; protein; 500 AA.
DE Human secreted/transmembrane protein #35.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 886
ID ABU95553 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 887
ID ABU96762 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 888

ID ABR70607 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 889
ID ABO04958 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 890
ID ABO08366 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 891
ID ABO05573 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 892
ID ABR73962 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 893
ID ABR95554 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 894
ID ABR80851 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 895
ID ABR81156 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 896
ID ABM00852 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 897
ID ABR88454 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 898
ID ABM77275 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 899
ID ABO28759 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 900
ID ABO31504 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 901
ID ABM07921 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 902
ID ABO40401 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 903
ID ABO35826 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 904
ID ABO43965 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 905
ID ADA77822 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 906
ID ABM24760 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;

Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 907
ID ABO03028 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 908
ID ABR90284 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 909
ID ABM17198 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 910
ID ABR94944 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 911
ID ABR95249 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 912
ID ABO21487 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 913
ID ABR97751 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 914
ID ABR87539 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 915
ID ABM77580 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 916
ID ABM27810 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 917
ID ABM06091 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 918
ID ABM03597 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 919
ID ABM35048 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 920
ID ABM26285 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 921
ID ABO48067 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 922
ID ABR92809 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 923
ID ABO24570 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 924
ID ABM11581 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 925
ID ABM02682 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073184-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 926
ID ABM15978 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 927
ID ABO27539 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 928
ID ABM29030 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 929
ID ABM07006 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 930
ID ABM21100 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 931
ID ABM09446 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 932
ID ABO41316 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 933
ID ABO36131 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 934
ID ABO43660 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 935
ID ABM76360 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 936
ID ABM76056 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 937
ID ABM25675 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 938
ID ABM25980 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 939
ID ABO03333 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 940
ID ABO02418 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 941
ID ABR90589 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 942
ID ABR73657 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 943
ID ABO16909 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 944
ID ABR94334 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003044917-A1.
PD 06-MAR-2003.

Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 945
ID ABR75841 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 946
ID ABR71217 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 947
ID ABR93114 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 948
ID ABR93419 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 949
ID ABR87844 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 950
ID ABO27844 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 951
ID ABO29979 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 952
ID ABO33188 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 953
ID ABM04876 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 954
ID ABM08836 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 955
ID ABO36436 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 956
ID ABO35521 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 957
ID ABO39486 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 958
ID ABM10361 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 959
ID ABM11886 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 960
ID ABO52032 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 961
ID ABO52337 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 962
ID ABO23655 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 963
ID ABR97141 standard; protein; 500 AA.

DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 964
ID ABR86929 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 965
ID ABM10971 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 966
ID ABM28115 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 967
ID ABO32114 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 968
ID ABM15241 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 969
ID ABM06396 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 970
ID ABM04207 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 971
ID ABM22320 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 972
ID ABM07616 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 973
ID ABO40706 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 974
ID ABM35353 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 975
ID ABM33116 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 976
ID ABO52642 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 977
ID ABO50202 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 978
ID ABU99196 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 979
ID ABO04248 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 980
ID ABO05878 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 981
ID ABM18418 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;

RESULT 982
ID ABR97446 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 983
ID ABR80546 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 984
ID ABM01157 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 985
ID ABR88759 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 986
ID ABM13411 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 987
ID ABM20795 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 988
ID ABO41926 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 989
ID ABO42536 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 990
ID ABM10056 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 991
ID ABO38571 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 992
ID ABM32811 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 993
ID ABM22625 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 994
ID ABM74836 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 995
ID ADA79614 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 996
ID ADA24902 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 997
ID ABR96226 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 998
ID ABM02377 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 999
ID ABR86319 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1000
ID ABR86624 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;

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  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1001
ID   ABM16588 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003064448-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1002
ID   ABM29640 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003064456-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1003
ID   ABO29064 standard; protein; 500 AA.
DE   Human secreted/transmembrane protein (PRO) #35.
PN   US2003068693-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1004
ID   ABM23845 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003068735-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1005
ID   ABM23235 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003068753-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1006
ID   ABM22015 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003068742-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1007
ID   ABO37656 standard; protein; 500 AA.
DE   Human secreted/transmembrane protein (PRO) #35.
PN   US2003068756-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1008
ID   ABM28420 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003082715-A1.
PD   01-MAY-2003.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1009
ID   ABM28725 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003082716-A1.
PD   01-MAY-2003.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1010
ID   ABM66369 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003068737-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1011
ID   ABM75751 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003104547-A1.
PD   05-JUN-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1012
ID   ABM34031 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003096359-A1.
PD   22-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1013
ID   ABM34336 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003100061-A1.
PD   29-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1014
ID   ABO19695 standard; protein; 500 AA.
DE   Novel human secreted and transmembrane protein PRO541.
PN   US2003050240-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1015
ID   ABO20267 standard; protein; 500 AA.
DE   Human secreted/transmembrane protein (PRO) #35.
PN   US2003032125-A1.
PD   13-FEB-2003.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1016
ID   ABO21182 standard; protein; 500 AA.
DE   Human secreted/transmembrane protein (PRO) #35.
PN   US2003054454-A1.
PD   20-MAR-2003.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1017
ID   ABO22097 standard; protein; 500 AA.
DE   Human secreted/transmembrane protein (PRO) #35.
PN   US2003054477-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1018
ID   ADA12563 standard; protein; 500 AA.
DE   Human secreted/transmembrane polypeptide PRO541.
PN   US2003055216-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 6;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1019
ID   ABR96531 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003054460-A1.
PD   20-MAR-2003.
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PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1020
ID ABR85709 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1021
ID ABR99691 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1022
ID ABM00242 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1023
ID ABM00547 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1024
ID ABO29674 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1025
ID ABM23540 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1026
ID ABM29335 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1027
ID ABO38266 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1028
ID ABO45566 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;

RESULT 1029
ID ABM20490 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1030
ID ADA81341 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1031
ID ABO16604 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1032
ID ABO18230 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1033
ID ABO22657 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1034
ID ABO22962 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1035
ID ABR92504 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1036
ID ABR81461 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1037
ID ABM77885 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1038
ID ABR89674 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073171-A1.

PD 17-APR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1039
ID ABM26590 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1040
ID ABM13716 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1041
ID ABO28454 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1042
ID ABO30284 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1043
ID ABM07311 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1044
ID ABM03902 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1045
ID ABO37046 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1046
ID ABO41621 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1047
ID ABO35216 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1048
ID ABM25065 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1049
ID ABO47457 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1050
ID ABO47762 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1051
ID ABO48372 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1052
ID ABO51422 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1053
ID ABO51727 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1054
ID ABO50507 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1055
ID ABR79631 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1056
ID ABM16893 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1057
ID ABO17925 standard; protein; 500 AA.

DE Human secreted/transmembrane protein (PRO) #35.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1058
ID ABO20877 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1059
ID ABR96836 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1060
ID ABM12191 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1061
ID ABM16283 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1062
ID ABM24150 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1063
ID ABM14631 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1064
ID ABM04512 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1065
ID ABM06701 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1066
ID ABM09141 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1067
ID ABO39181 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1068
ID ABM75446 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1069
ID ABM25370 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1070
ID ABM19880 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1071
ID ABO46786 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1072
ID ABO47091 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1073
ID ADA83139 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1074
ID ABR71522 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1075
ID ABR72132 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1076
ID ABR98471 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.

PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1077
ID ABO06841 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1078
ID ABR84794 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1079
ID ABR73352 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1080
ID ABR76446 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1081
ID ABR73047 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1082
ID ABM18113 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1083
ID ABO20572 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1084
ID ABO25315 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1085
ID ABO25620 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1086
ID ABR94029 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1087
ID ABR79936 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1088
ID ABM11276 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1089
ID ABO32883 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1090
ID ABO30589 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1091
ID ABO30894 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1092
ID ABM27200 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1093
ID ABM29945 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1094
ID ABM05481 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1095
ID ABM15546 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068698-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1096
ID ABM08531 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1097
ID ABO42231 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1098
ID ABO37961 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1099
ID ABO45871 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1100
ID ABM66674 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1101
ID ADB20182 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003082767-A1.
PD 01-MAY-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1102
ID ABM19575 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1103
ID ABO49287 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1104
ID ABO49592 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1105
ID ADA78434 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1106
ID ABO19586 standard; protein; 500 AA.
DE Novel human secreted and transmembrane polypeptide #54.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1107
ID ABR88149 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1108
ID ABM26895 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1109
ID ABM03292 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1110
ID ABO39791 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 6; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1111
ID ABO49897 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1112
ID ABO50812 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1113
ID ABO05268 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1114

ID ABR74572 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1115
ID ABR77051 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1116
ID ABM17808 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1117
ID ABR95859 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1118
ID ABO21792 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1119
ID ABO19962 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1120
ID ABO24265 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1121
ID ABR86014 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1122
ID ABM10666 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1123
ID ABM76665 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1124
ID ABR89369 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1125
ID ABM12496 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1126
ID ABM05786 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1127
ID ABO34911 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1128
ID ABM02987 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1129
ID ABM18965 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1130
ID ABM19270 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1131
ID ABO46481 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1132
ID ABO48982 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1133

ID ABR69025 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1134
ID ABR89064 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1135
ID ABR72437 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1136
ID ABR74267 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1137
ID ABO18535 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1138
ID ABR80241 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1139
ID ABM01462 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1140
ID ABM02072 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1141
ID ABR87234 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1142
ID ABM12801 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1143
ID ABM30555 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1144
ID ABM24455 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1145
ID ABO29369 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1146
ID ABO31199 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1147
ID ABM14326 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1148
ID ABM09751 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1149
ID ABO38876 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1150
ID ABM34641 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1151
ID ABO51117 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;

RESULT 1152
ID ABO03943 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1153
ID ABO10413 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1154
ID ABR77656 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1155
ID ABR78866 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1156
ID ABO23960 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1157
ID ABR93724 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1158
ID ABM01767 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1159
ID ABM78190 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1160
ID ABR89979 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1161
ID ABM27505 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1162
ID ABM13106 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1163
ID ABO31809 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1164
ID ABM14021 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1165
ID ABM08226 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1166
ID ABO40096 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1167
ID ABM74531 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1168
ID ABM33726 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1169
ID ABM20185 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1170
ID ABO48677 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;

RESULT 1171
ID ABR72742 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1172
ID ABO15384 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1173
ID ABR85099 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1174
ID ABO15079 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1175
ID ABO17214 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1176
ID ABM17503 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1177
ID ABR85404 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1178
ID ABM76970 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1179
ID ABO28149 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1180
ID ABM22930 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1181
ID ABM30250 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1182
ID ABM21710 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1183
ID ABM21405 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1184
ID ABM14936 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1185
ID ABO41011 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1186
ID ABO36741 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1187
ID ABO37351 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1188
ID ABM75141 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1189
ID ABM33421 standard; protein; 500 AA.
DE Human secreted polypeptide PRO541, SEQ ID NO:70.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;

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  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1190
ID   ABO46176 standard; protein; 500 AA.
DE   Human PRO polypeptide #35.
PN   US2003049760-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1191
ID   ADA82505 standard; protein; 500 AA.
DE   Human secreted/transmembrane protein (PRO) #35.
PN   US2003049755-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1192
ID   ABM31775 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003068680-A1.
PD   10-APR-2003.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1193
ID   ABM31165 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003068762-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1194
ID   ADB73869 standard; protein; 500 AA.
DE   Human PRO polypeptide #54.
PN   US2003045462-A1.
PD   06-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1195
ID   ADB85813 standard; protein; 500 AA.
DE   Human secreted/transmembrane protein (PRO) #35.
PN   US2003054472-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1196
ID   ABM32080 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003068708-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1197
ID   ABM32385 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003068713-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1198
ID   ABM31470 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003068761-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1199
ID   ABM30860 standard; protein; 500 AA.
DE   Human secreted polypeptide PRO541, SEQ ID NO:70.
PN   US2003068771-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1200
ID   ADB76585 standard; protein; 500 AA.
DE   Human PRO polypeptide #54.
PN   US2003083248-A1.
PD   01-MAY-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1201
ID   ADC44011 standard; protein; 500 AA.
DE   Human secreted/transmembrane protein, PRO541.
PN   US2003054986-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1202
ID   ADC61771 standard; protein; 500 AA.
DE   Human secreted/transmembrane protein, PRO541.
PN   US2003049684-A1.
PD   13-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1203
ID   ADC63735 standard; protein; 500 AA.
DE   Human secreted/transmembrane protein, PRO541.
PN   US2003054405-A1.
PD   20-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1204
ID   ADC66835 standard; protein; 500 AA.
DE   Human secreted/transmembrane protein, PRO541.
PN   US2003060406-A1.
PD   27-MAR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1205
ID   ADC68959 standard; protein; 500 AA.
DE   Human secreted/transmembrane protein, PRO541.
PN   US2003064407-A1.
PD   03-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1206
ID   ADC63019 standard; protein; 500 AA.
DE   Human secreted/transmembrane protein, PRO541.
PN   US2003068648-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1207
ID   ADC68084 standard; protein; 500 AA.
DE   Human secreted/transmembrane protein, PRO541.
PN   US2003069178-A1.
PD   10-APR-2003.
PA   (GETH ) GENENTECH INC.
  Query Match             9.3%;  Score 235.5;  DB 7;  Length 500;
  Best Local Similarity   24.5%;  Pred. No. 3.7e-09;
RESULT 1208
ID   ADC41404 standard; protein; 500 AA.
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DE Human secreted/transmembrane protein, PRO541.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1209
ID ADC67459 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1210
ID ADC62395 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1211
ID ADC42028 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1212
ID ADD05543 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1213
ID ADE49397 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1214
ID ADE35451 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1215
ID ADE16565 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1216
ID ADD73180 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1217
ID ADD72538 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1218
ID ADE17189 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1219
ID ADF47203 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1220
ID ADG02538 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1221
ID ADG01245 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1222
ID ADF95420 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1223
ID ADG12235 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1224
ID ADH08895 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1225
ID ADG52960 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1226
ID ADG60280 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003206915-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1227
ID ADI61040 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1228
ID ADL32676 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1229
ID ADM30210 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 7; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1230
ID ADE48697 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1231
ID ADE74207 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1232
ID ADE74819 standard; protein; 500 AA.
DE Human secreted/transmembrane protein (PRO) #35.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1233
ID ADE89798 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1234
ID ADF61438 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1235
ID ADF40130 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1236
ID ADF45926 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1237
ID ADF24322 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1238
ID ADF40754 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1239
ID ADF23698 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1240
ID ADF33681 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1241
ID ADF27148 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;

Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1242
ID ADF27784 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1243
ID ADF41378 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1244
ID ADF33057 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1245
ID ADF25423 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1246
ID ADF26524 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1247
ID ADF34313 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1248
ID ADF46550 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1249
ID ADF96032 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1250
ID ADG04303 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1251
ID ADG00463 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1252
ID ADG82719 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1253
ID ADH26000 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1254
ID ADG50536 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1255
ID ADG49912 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1256
ID ADG51784 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1257
ID ADH32969 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1258
ID ADG49288 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1259
ID ADG48664 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1260
ID ADG51160 standard; protein; 500 AA.

DE Human secreted/transmembrane protein, PRO541.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1261
ID ADG59104 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1262
ID ADG62560 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1263
ID ADH25585 standard; protein; 500 AA.
DE Human neurotrimin homologue related protein sequence SEQ ID NO:363.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1264
ID ADJ54708 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1265
ID ADJ64479 standard; protein; 500 AA.
DE Human PRO polypeptide #35.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1266
ID ADM31375 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1267
ID ADM17362 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1268
ID ADM36422 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1269
ID ADM40227 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1270
ID ADL07196 standard; protein; 500 AA.
DE Human secreted/transmembrane protein, PRO541.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1271
ID ADN37835 standard; protein; 500 AA.
DE Novel human secreted and transmembrane protein PRO541.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 9.3%; Score 235.5; DB 8; Length 500;
Best Local Similarity 24.5%; Pred. No. 3.7e-09;
RESULT 1272
ID AAM41693 standard; protein; 522 AA.
DE Human polypeptide SEQ ID NO 6624.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.3%; Score 235.5; DB 4; Length 522;
Best Local Similarity 24.5%; Pred. No. 3.9e-09;
RESULT 1273
ID ABR56795 standard; protein; 500 AA.
DE Human secreted protein SECP-70 SEQ ID NO:70.
PN WO2003016506-A2.
PD 27-FEB-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 9.3%; Score 234.5; DB 6; Length 500;
Best Local Similarity 23.8%; Pred. No. 4.4e-09;
RESULT 1274
ID ADB32041 standard; protein; 300 AA.
DE Human FCTR7 polypeptide.
PN US2003087816-A1.
PD 08-MAY-2003.
PA (VERM/) VERMET C.
PA (FERN/) FERNANDES E.
PA (SHIM/) SHIMKETS R.
PA (HERR/) HERRMANN J.
PA (MAJU/) MAJUMDER K.
PA (MACD/) MACDOUGALL J.
PA (MISH/) MISHRA V.
PA (MEZE/) MEZES P S.
PA (RAST/) RASTELLI L.
Query Match 9.3%; Score 234; DB 7; Length 300;
Best Local Similarity 34.2%; Pred. No. 2.7e-09;
RESULT 1275
ID AAE09683 standard; protein; 277 AA.
DE Human gene 1 encoded novel protein HTPGQ16, SEQ ID NO:17.
PN WO200155310-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.2%; Score 233.5; DB 4; Length 277;
Best Local Similarity 31.6%; Pred. No. 2.7e-09;
RESULT 1276
ID ABU10131 standard; protein; 277 AA.
DE Human serine protease inhibitor related protein #1.
PN US2003044905-A1.
PD 06-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.2%; Score 233.5; DB 6; Length 277;
Best Local Similarity 31.6%; Pred. No. 2.7e-09;
RESULT 1277
ID AAU20491 standard; protein; 268 AA.
DE Human secreted protein, Seq ID No 483.
PN WO200155326-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.2%; Score 233; DB 4; Length 268;
Best Local Similarity 34.2%; Pred. No. 2.8e-09;
RESULT 1278
ID AAM39907 standard; protein; 300 AA.
DE Human polypeptide SEQ ID NO 3052.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 9.2%; Score 233; DB 4; Length 300;
Best Local Similarity 34.2%; Pred. No. 3.2e-09;
RESULT 1279
ID AAB64952 standard; protein; 181 AA.
DE Gene 12 human secreted protein homologous amino acid sequence #130.
PN WO200076530-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 9.2%; Score 232; DB 4; Length 181;
Best Local Similarity 32.4%; Pred. No. 2.2e-09;
RESULT 1280
ID AAB01400 standard; protein; 219 AA.
DE Neuron-associated protein.
PN WO200034477-A2.
PD 15-JUN-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 9.2%; Score 232; DB 3; Length 219;
Best Local Similarity 32.4%; Pred. No. 2.7e-09;
RESULT 1281
ID ADH54571 standard; protein; 219 AA.
DE Human LRF-1 related protein from clone HTEIX55R.
PN US2003162956-A1.
PD 28-AUG-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.2%; Score 232; DB 7; Length 219;
Best Local Similarity 32.4%; Pred. No. 2.7e-09;
RESULT 1282
ID ADP12924 standard; protein; 266 AA.
DE Protein encoding referenece mRNA sequence #9.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 9.1%; Score 231; DB 8; Length 266;
Best Local Similarity 32.4%; Pred. No. 3.9e-09;
RESULT 1283
ID ADQ17660 standard; protein; 266 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 477.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 9.1%; Score 231; DB 8; Length 266;
Best Local Similarity 32.4%; Pred. No. 3.9e-09;
RESULT 1284
ID ADQ96006 standard; protein; 266 AA.
DE T cell activation associated protein #92.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 9.1%; Score 231; DB 8; Length 266;
Best Local Similarity 32.4%; Pred. No. 3.9e-09;
RESULT 1285
ID ADQ96004 standard; protein; 266 AA.
DE T cell activation associated protein #91.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 9.1%; Score 231; DB 8; Length 266;
Best Local Similarity 32.4%; Pred. No. 3.9e-09;
RESULT 1286
ID ADQ95960 standard; protein; 266 AA.
DE T cell activation associated protein #69.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 9.1%; Score 231; DB 8; Length 266;
Best Local Similarity 32.4%; Pred. No. 3.9e-09;
RESULT 1287
ID ADP54490 standard; protein; 266 AA.
DE Human PRO protein sequence SEQ ID NO:466.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 9.1%; Score 231; DB 8; Length 266;
Best Local Similarity 32.4%; Pred. No. 3.9e-09;
RESULT 1288
ID ADE86027 standard; protein; 236 AA.
DE Mouse sperm polypeptide CRISPY.
PN WO2003087151-A1.
PD 23-OCT-2003.
PA (MONU) UNIV MONASH.
Query Match 8.9%; Score 225; DB 7; Length 236;
Best Local Similarity 34.5%; Pred. No. 9.7e-09;
RESULT 1289
ID ADF74788 standard; protein; 243 AA.
DE Human NOVX protein to treat human pathological conditions (SeqID 2).
PN WO2003076578-A2.
PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.8%; Score 223; DB 7; Length 243;
Best Local Similarity 28.6%; Pred. No. 1.4e-08;
RESULT 1290
ID ABG06656 standard; protein; 257 AA.
DE Novel human diagnostic protein #6647.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.8%; Score 222.5; DB 4; Length 257;
Best Local Similarity 27.9%; Pred. No. 1.6e-08;
RESULT 1291
ID ADD13128 standard; protein; 243 AA.
DE Human TPX1 protein SEQ ID 41.
PN WO2003076631-A2.
PD 18-SEP-2003.
PA (SAHI/) SAHIN U.
PA (TUER/) TUERECI O.
PA (KOSL/) KOSLOWSKI M.
Query Match 8.7%; Score 221; DB 7; Length 243;
Best Local Similarity 28.1%; Pred. No. 2e-08;
RESULT 1292
ID ADE94307 standard; protein; 243 AA.
DE Human cysteine-rich secretory protein 2 SEQ ID NO:4.
PN WO2003100025-A2.
PD 04-DEC-2003.
PA (MINU) UNIV MINNESOTA.
PA (HAMI/) HAMILTON D W.
PA (ROBE/) ROBERTS K P.
PA (ENSR/) ENSRUD K M.
Query Match 8.7%; Score 221; DB 8; Length 243;
Best Local Similarity 28.1%; Pred. No. 2e-08;
RESULT 1293
ID AAB43408 standard; protein; 302 AA.
DE Human cancer associated protein sequence SEQ ID NO:853.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.7%; Score 220; DB 3; Length 302;
Best Local Similarity 31.8%; Pred. No. 3e-08;
RESULT 1294
ID AAE13072 standard; protein; 243 AA.
DE Homo sapiens (Hs)-Tpx protein.
PN WO200174385-A1.
PD 11-OCT-2001.
PA (NYBL-) NEW YORK BLOOD CENT INC.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
PA (UABR-) UAB RES FOUND.

Query Match 8.7%; Score 219; DB 4; Length 243;
Best Local Similarity 27.7%; Pred. No. 2.8e-08;
RESULT 1295
ID AAR46627 standard; protein; 1257 AA.
DE Neurocan core protein.
PN WO9403601-A2.
PD 17-FEB-1994.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.5%; Score 214; DB 2; Length 1257;
Best Local Similarity 24.8%; Pred. No. 4.3e-07;
RESULT 1296
ID ADE94304 standard; protein; 249 AA.
DE Human cysteine-rich secretory protein 1 SEQ ID NO:1.
PN WO2003100025-A2.
PD 04-DEC-2003.
PA (MINU) UNIV MINNESOTA.
PA (HAMI/) HAMILTON D W.
PA (ROBE/) ROBERTS K P.
PA (ENSR/) ENSRUD K M.
Query Match 8.4%; Score 213.5; DB 8; Length 249;
Best Local Similarity 27.2%; Pred. No. 7.5e-08;
RESULT 1297
ID ADH71214 standard; protein; 453 AA.
DE Human protein of the invention NOV6o SEQ ID NO:110.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.4%; Score 212.5; DB 8; Length 453;
Best Local Similarity 23.4%; Pred. No. 1.7e-07;
RESULT 1298
ID ADO31200 standard; protein; 1257 AA.
DE Rat neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 8.4%; Score 212; DB 8; Length 1257;
Best Local Similarity 24.8%; Pred. No. 6e-07;
RESULT 1299
ID ADE94306 standard; protein; 244 AA.
DE Mouse cysteine-rich secretory protein 1 SEQ ID NO:3.
PN WO2003100025-A2.
PD 04-DEC-2003.
PA (MINU) UNIV MINNESOTA.
PA (HAMI/) HAMILTON D W.
PA (ROBE/) ROBERTS K P.
PA (ENSR/) ENSRUD K M.
Query Match 8.3%; Score 209; DB 8; Length 244;
Best Local Similarity 25.7%; Pred. No. 1.6e-07;
RESULT 1300
ID ADD48595 standard; protein; 656 AA.
DE Rat Protein AF072892, SEQ ID NO 14301.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 8.3%; Score 209; DB 7; Length 656;
Best Local Similarity 27.5%; Pred. No. 4.9e-07;
RESULT 1301
ID ADE94308 standard; protein; 243 AA.
DE Rat cysteine-rich secretory protein 2 SEQ ID NO:5.
PN WO2003100025-A2.
PD 04-DEC-2003.
PA (MINU) UNIV MINNESOTA.
PA (HAMI/) HAMILTON D W.
PA (ROBE/) ROBERTS K P.
PA (ENSR/) ENSRUD K M.
Query Match 8.2%; Score 207.5; DB 8; Length 243;
Best Local Similarity 25.9%; Pred. No. 2.1e-07;
RESULT 1302
ID AAM52242 standard; protein; 655 AA.
DE Human versican isoform V3 SEQ ID NO 2.
PN WO200179284-A2.
PD 25-OCT-2001.
PA (WIGH/) WIGHT T N.
PA (MERR/) MERRILEES M.
Query Match 8.1%; Score 205; DB 5; Length 655;
Best Local Similarity 27.1%; Pred. No. 9.7e-07;
RESULT 1303
ID ADQ39511 standard; protein; 655 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1174.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 8.1%; Score 205; DB 8; Length 655;
Best Local Similarity 27.1%; Pred. No. 9.7e-07;
RESULT 1304
ID ABP97200 standard; protein; 1321 AA.
DE Tumour-associated antigenic target protein TAT185 SEQ ID NO:82.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 8.1%; Score 205; DB 6; Length 1321;
Best Local Similarity 21.3%; Pred. No. 2.1e-06;
RESULT 1305
ID ADJ69615 standard; protein; 1321 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1421.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 8.1%; Score 205; DB 7; Length 1321;
Best Local Similarity 21.3%; Pred. No. 2.1e-06;
RESULT 1306
ID ADN38944 standard; protein; 1321 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:262.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.1%; Score 205; DB 7; Length 1321;
Best Local Similarity 21.3%; Pred. No. 2.1e-06;
RESULT 1307
ID ADO31196 standard; protein; 1321 AA.
DE Human neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 8.1%; Score 205; DB 8; Length 1321;
Best Local Similarity 21.3%; Pred. No. 2.1e-06;
RESULT 1308
ID ADH71212 standard; protein; 453 AA.
DE Human protein of the invention NOV6n SEQ ID NO:108.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 204.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 6.9e-07;
RESULT 1309
ID ADH71216 standard; protein; 453 AA.
DE Human protein of the invention NOV6p SEQ ID NO:112.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 204.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 6.9e-07;
RESULT 1310
ID ADH71186 standard; protein; 453 AA.
DE Human protein of the invention NOV6a SEQ ID NO:82.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 204.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 6.9e-07;
RESULT 1311
ID ADH71188 standard; protein; 457 AA.
DE Human protein of the invention NOV6b SEQ ID NO:84.
PN WO2003102155-A2.

PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.1%; Score 204.5; DB 8; Length 457;
Best Local Similarity 22.6%; Pred. No. 7e-07;
RESULT 1312
ID ADH71210 standard; protein; 453 AA.
DE Human protein of the invention NOV6m SEQ ID NO:106.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 8.0%; Score 203.5; DB 8; Length 453;
Best Local Similarity 23.1%; Pred. No. 8.3e-07;
RESULT 1313
ID ABM85041 standard; protein; 452 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5290.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.0%; Score 203; DB 8; Length 452;
Best Local Similarity 23.1%; Pred. No. 9e-07;
RESULT 1314
ID ADJ76266 standard; protein; 2397 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1518.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 7.9%; Score 200; DB 8; Length 2397;
Best Local Similarity 27.0%; Pred. No. 9.9e-06;
RESULT 1315
ID ABP96842 standard; peptide; 31 AA.
DE Human PREGF peptide 231-261.
PN CN1366046-A.
PD 28-AUG-2002.
PA (UYFU-) UNIV FUDAN.
Query Match 7.9%; Score 199; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.7e-08;
RESULT 1316
ID ABB71656 standard; protein; 380 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41760.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.8%; Score 196.5; DB 4; Length 380;
Best Local Similarity 32.2%; Pred. No. 2.3e-06;
RESULT 1317
ID ADH71208 standard; protein; 453 AA.
DE Human protein of the invention NOV6l SEQ ID NO:104.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.8%; Score 196.5; DB 8; Length 453;
Best Local Similarity 22.8%; Pred. No. 2.8e-06;
RESULT 1318
ID AAB43485 standard; protein; 741 AA.
DE Human cancer associated protein sequence SEQ ID NO:930.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.8%; Score 196; DB 3; Length 741;
Best Local Similarity 26.8%; Pred. No. 5.2e-06;
RESULT 1319
ID ADQ39513 standard; protein; 1642 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1176.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.8%; Score 196; DB 8; Length 1642;
Best Local Similarity 26.8%; Pred. No. 1.3e-05;
RESULT 1320
ID ADQ39515 standard; protein; 1642 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1178.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.8%; Score 196; DB 8; Length 1642;
Best Local Similarity 26.8%; Pred. No. 1.3e-05;
RESULT 1321
ID AAR12609 standard; protein; 2409 AA.
DE Versican.
PN WO9108230-A.
PD 13-JUN-1991.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 7.8%; Score 196; DB 2; Length 2409;
Best Local Similarity 26.8%; Pred. No. 2e-05;
RESULT 1322
ID ABR47429 standard; protein; 2409 AA.
DE Breast cancer associated protein sequence SEQ ID NO:90.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 7.8%; Score 196; DB 6; Length 2409;
Best Local Similarity 26.8%; Pred. No. 2e-05;
RESULT 1323
ID ADQ39514 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1177.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.8%; Score 196; DB 8; Length 2409;
Best Local Similarity 26.8%; Pred. No. 2e-05;
RESULT 1324
ID ADQ39512 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1175.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.8%; Score 196; DB 8; Length 2409;
Best Local Similarity 26.8%; Pred. No. 2e-05;
RESULT 1325
ID ADJ70171 standard; protein; 3024 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1977.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 7.8%; Score 196; DB 7; Length 3024;
Best Local Similarity 26.8%; Pred. No. 2.6e-05;
RESULT 1326
ID ADD48597 standard; protein; 3396 AA.
DE Human Protein P13611, SEQ ID NO 14303.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.8%; Score 196; DB 7; Length 3396;
Best Local Similarity 26.8%; Pred. No. 2.9e-05;
RESULT 1327
ID ADN95526 standard; protein; 3396 AA.
DE Human BEC/LEC-related protein sequence SeqID449.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 7.8%; Score 196; DB 7; Length 3396;
Best Local Similarity 26.8%; Pred. No. 2.9e-05;
RESULT 1328
ID ADJ75521 standard; protein; 3396 AA.
DE Marker gene related amino acid sequence SEQ ID NO:773.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 7.8%; Score 196; DB 8; Length 3396;
Best Local Similarity 26.8%; Pred. No. 2.9e-05;
RESULT 1329
ID ADQ39509 standard; protein; 3396 AA.

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1172.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.8%; Score 196; DB 8; Length 3396;
Best Local Similarity 26.8%; Pred. No. 2.9e-05;
RESULT 1330
ID ADQ39510 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1173.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.8%; Score 196; DB 8; Length 3396;
Best Local Similarity 26.8%; Pred. No. 2.9e-05;
RESULT 1331
ID ADR99164 standard; protein; 3396 AA.
DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, SEQ ID 170.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 7.8%; Score 196; DB 8; Length 3396;
Best Local Similarity 26.8%; Pred. No. 2.9e-05;
RESULT 1332
ID ABG08950 standard; protein; 412 AA.
DE Novel human diagnostic protein #8941.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.7%; Score 194.5; DB 4; Length 412;
Best Local Similarity 35.0%; Pred. No. 3.5e-06;
RESULT 1333
ID AAM48742 standard; protein; 203 AA.
DE Maize PR1-C10 SEQ ID NO 2.
PN US2001049834-A1.
PD 06-DEC-2001.
PA (CRAN/) CRANE E H.
PA (CRAN/) CRANE V C.
Query Match 7.7%; Score 193.5; DB 5; Length 203;
Best Local Similarity 31.3%; Pred. No. 1.9e-06;
RESULT 1334
ID ADH54566 standard; protein; 279 AA.
DE Human leukocyte regulatory factor (LRF)-1 protein.
PN US2003162956-A1.
PD 28-AUG-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.5%; Score 190.5; DB 7; Length 279;
Best Local Similarity 28.6%; Pred. No. 4.5e-06;
RESULT 1335
ID AAB23824 standard; protein; 1455 AA.
DE Murine macrophage mannose receptor protein SEQ ID NO:5.
PN US6117977-A.
PD 12-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 7.5%; Score 189.5; DB 2; Length 1455;
Best Local Similarity 23.3%; Pred. No. 3.4e-05;
RESULT 1336
ID ABP81196 standard; protein; 161 AA.
DE Arabidopsis thaliana protein #24 modulated by PTGS.
PN WO200281695-A2.
PD 17-OCT-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (FRIE-) FRIEDRICH MIESCHER INST.
Query Match 7.3%; Score 185.5; DB 6; Length 161;
Best Local Similarity 30.2%; Pred. No. 5.7e-06;
RESULT 1337
ID ABP69108 standard; protein; 253 AA.
DE Human polypeptide SEQ ID NO 1155.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.3%; Score 185; DB 5; Length 253;
Best Local Similarity 27.9%; Pred. No. 1e-05;
RESULT 1338
ID AAE27986 standard; protein; 586 AA.
DE Human EGF-family protein #2.
PN WO200272611-A2.
PD 19-SEP-2002.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.3%; Score 184.5; DB 5; Length 586;
Best Local Similarity 28.6%; Pred. No. 2.9e-05;
RESULT 1339
ID AAE27985 standard; protein; 1140 AA.
DE Human EGF-family protein #1.
PN WO200272611-A2.
PD 19-SEP-2002.
PA (LEXI-) LEXICON GENETICS INC.
Query Match 7.3%; Score 184.5; DB 5; Length 1140;
Best Local Similarity 28.6%; Pred. No. 6.2e-05;
RESULT 1340
ID ADD18688 standard; protein; 1140 AA.
DE Human disease related protein SeqID119.
PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 7.3%; Score 184.5; DB 7; Length 1140;
Best Local Similarity 28.6%; Pred. No. 6.2e-05;
RESULT 1341
ID ADJ70032 standard; protein; 1140 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1838.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 7.3%; Score 184.5; DB 7; Length 1140;
Best Local Similarity 28.6%; Pred. No. 6.2e-05;
RESULT 1342
ID ADS11010 standard; protein; 1140 AA.
DE Human therapeutic protein - SEQ ID 1247.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.3%; Score 184.5; DB 8; Length 1140;
Best Local Similarity 28.6%; Pred. No. 6.2e-05;
RESULT 1343
ID ADE71305 standard; protein; 1192 AA.
DE Novel human protein #59.
PN JP2002345493-A.
PD 03-DEC-2002.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 7.3%; Score 184.5; DB 7; Length 1192;
Best Local Similarity 28.6%; Pred. No. 6.5e-05;
RESULT 1344
ID ADF74179 standard; protein; 1192 AA.
DE Human novel brain/hippocampus protein #67.
PN JP2003009886-A.
PD 14-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (PROT-) PROTEIN EXPRESS KK.
Query Match 7.3%; Score 184.5; DB 7; Length 1192;
Best Local Similarity 28.6%; Pred. No. 6.5e-05;
RESULT 1345
ID AAU32663 standard; protein; 673 AA.
DE Novel human secreted protein #3154.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.2%; Score 183; DB 4; Length 673;
Best Local Similarity 30.9%; Pred. No. 4.4e-05;
RESULT 1346
ID AAY43998 standard; protein; 135 AA.
DE Tobacco pathogenesis related protein #1.
PN US5958784-A.
PD 28-SEP-1999.
PA (BENN/) BENNER S A.
Query Match 7.2%; Score 182.5; DB 2; Length 135;
Best Local Similarity 33.3%; Pred. No. 7.9e-06;

RESULT 1347
ID AAY43999 standard; protein; 135 AA.
DE Tomato pathogenesis related protein #1.
PN US5958784-A.
PD 28-SEP-1999.
PA (BENN/) BENNER S A.
Query Match 7.2%; Score 182.5; DB 2; Length 135;
Best Local Similarity 33.3%; Pred. No. 7.9e-06;
RESULT 1348
ID AAR28350 standard; protein; 159 AA.
DE Pathogenesis-related protein P14a isolated from tomato.
PN WO9220800-A1.
PD 26-NOV-1992.
PA (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
Query Match 7.2%; Score 182.5; DB 2; Length 159;
Best Local Similarity 33.3%; Pred. No. 9.5e-06;
RESULT 1349
ID ABB77766 standard; protein; 162 AA.
DE Amino acid sequence of an antibacterial protein.
PN JP2002095475-A.
PD 02-APR-2002.
PA (IWAT-) IWATE KEN.
Query Match 7.2%; Score 182.5; DB 5; Length 162;
Best Local Similarity 31.6%; Pred. No. 9.7e-06;
RESULT 1350
ID AAB64953 standard; protein; 178 AA.
DE Human secreted protein sequence encoded by gene 12 SEQ ID NO:131.
PN WO200076530-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 7.2%; Score 182.5; DB 4; Length 178;
Best Local Similarity 30.2%; Pred. No. 1.1e-05;
RESULT 1351
ID AAR28354 standard; protein; 159 AA.
DE Pathogenesis-related protein P14f isolated from tomato.
PN WO9220800-A1.
PD 26-NOV-1992.
PA (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
Query Match 7.2%; Score 181.5; DB 2; Length 159;
Best Local Similarity 31.8%; Pred. No. 1.1e-05;
RESULT 1352
ID ADB65314 standard; protein; 229 AA.
DE Human protein encoded by clone TESTI20071630.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.2%; Score 181.5; DB 7; Length 229;
Best Local Similarity 30.2%; Pred. No. 1.7e-05;
RESULT 1353
ID ADK68232 standard; protein; 343 AA.
DE Novel NOVX protein #79.
PN WO2003085124-A2.
PD 16-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.2%; Score 181.5; DB 7; Length 343;
Best Local Similarity 30.2%; Pred. No. 2.7e-05;
RESULT 1354
ID ADH72226 standard; protein; 343 AA.
DE Human protein of the invention NOV55a SEQ ID NO:1122.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.2%; Score 181.5; DB 8; Length 343;
Best Local Similarity 30.2%; Pred. No. 2.7e-05;
RESULT 1355
ID ADR49221 standard; protein; 343 AA.
DE Human NOV10a protein.
PN US2004162236-A1.
PD 19-AUG-2004.
PA (ALSO/) ALSOBROOK J.
PA (BENT/) BENTO P.
PA (BOLD/) BOLDOG F.
PA (BURG/) BURGESS C.
PA (CASM/) CASMAN S.
PA (BOKO/) BOKOR J C.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (FERN/) FERNANDES E.
PA (GERL/) GERLACH V.
PA (GROS/) GROSSE W.
PA (GUNT/) GUNTHER E.
PA (GUSE/) GUSEV V.
PA (HEYE/) HEYES M.
PA (LEPL/) LEPLEY D.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PATT/) PATTURAJAN M.
PA (PEYM/) PEYMAN J A.
PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENOY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match 7.2%; Score 181.5; DB 8; Length 343;
Best Local Similarity 30.2%; Pred. No. 2.7e-05;
RESULT 1356
ID AAY44000 standard; protein; 135 AA.
DE Tomato pathogenesis related protein #2.
PN US5958784-A.
PD 28-SEP-1999.
PA (BENN/) BENNER S A.
Query Match 7.1%; Score 180.5; DB 2; Length 135;
Best Local Similarity 33.3%; Pred. No. 1.1e-05;
RESULT 1357
ID AAR28351 standard; protein; 159 AA.
DE Pathogenesis-related protein P14b isolated from tomato.
PN WO9220800-A1.
PD 26-NOV-1992.
PA (SANO) SANDOZ LTD.
PA (SANO) SANDOZ PATENT GMBH.
Query Match 7.1%; Score 180.5; DB 2; Length 159;
Best Local Similarity 33.3%; Pred. No. 1.3e-05;
RESULT 1358
ID ABB77765 standard; protein; 161 AA.
DE Amino acid sequence of an antibacterial protein.
PN JP2002095475-A.
PD 02-APR-2002.
PA (IWAT-) IWATE KEN.
Query Match 7.1%; Score 180.5; DB 5; Length 161;
Best Local Similarity 31.1%; Pred. No. 1.4e-05;
RESULT 1359
ID AAG42365 standard; protein; 163 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52828.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.1%; Score 180.5; DB 3; Length 163;
Best Local Similarity 31.9%; Pred. No. 1.4e-05;
RESULT 1360
ID ABP81272 standard; protein; 163 AA.
DE Arabidopsis thaliana protein #100 modulated by PTGS.
PN WO200281695-A2.
PD 17-OCT-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (FRIE-) FRIEDRICH MIESCHER INST.
Query Match 7.1%; Score 180.5; DB 6; Length 163;
Best Local Similarity 31.9%; Pred. No. 1.4e-05;
RESULT 1361

ID AAW35693 standard; peptide; 205 AA.
DE Vespid antigen 5s from Polistes exclamans (wasp).
PN WO9733910-A1.
PD 18-SEP-1997.
PA (UYRQ) UNIV ROCKEFELLER.
Query Match 7.1%; Score 180.5; DB 2; Length 205;
Best Local Similarity 31.6%; Pred. No. 1.8e-05;
RESULT 1362
ID AAW35692 standard; peptide; 205 AA.
DE Vespid antigen 5s from Polistes annularis (wasp).
PN WO9733910-A1.
PD 18-SEP-1997.
PA (UYRQ) UNIV ROCKEFELLER.
Query Match 7.1%; Score 180.5; DB 2; Length 205;
Best Local Similarity 30.8%; Pred. No. 1.8e-05;
RESULT 1363
ID AAE28821 standard; protein; 205 AA.
DE Polistes annularis antigen 5 (Pol a5) allergen protein.
PN WO200270665-A2.
PD 12-SEP-2002.
PA (UYRQ) UNIV ROCKEFELLER.
PA (ALKA-) ALK-ABELLO AS.
Query Match 7.1%; Score 180.5; DB 5; Length 205;
Best Local Similarity 30.8%; Pred. No. 1.8e-05;
RESULT 1364
ID ADF74842 standard; protein; 2775 AA.
DE Murine NOVX protein to treat human pathological conditions (SeqID 56).
PN WO2003076578-A2.
PD 18-SEP-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.1%; Score 180.5; DB 7; Length 2775;
Best Local Similarity 27.8%; Pred. No. 0.00034;
RESULT 1365
ID ABP97463 standard; protein; 737 AA.
DE Mouse Delta/Notch-like EGF-related receptor (DNER).
PN WO2003029467-A1.
PD 10-APR-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 7.1%; Score 180; DB 6; Length 737;
Best Local Similarity 27.8%; Pred. No. 8.2e-05;
RESULT 1366
ID ABG20726 standard; protein; 1184 AA.
DE Novel human diagnostic protein #20717.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 178.5; DB 4; Length 1184;
Best Local Similarity 29.2%; Pred. No. 0.00018;
RESULT 1367
ID AAR24033 standard; protein; 1456 AA.
DE Soluble mannose receptor peptide.
PN WO9207579-A1.
PD 14-MAY-1992.
PA (CHIL-) CHILDRENS MEDICAL CENT.
Query Match 7.1%; Score 178.5; DB 2; Length 1456;
Best Local Similarity 29.2%; Pred. No. 0.00023;
RESULT 1368
ID ABU79121 standard; protein; 1456 AA.
DE Angiostatin DNA.
PN US2002177551-A1.
PD 28-NOV-2002.
PA (TERM/) TERMAN D S.
Query Match 7.1%; Score 178.5; DB 6; Length 1456;
Best Local Similarity 29.2%; Pred. No. 0.00023;
RESULT 1369
ID ADF43375 standard; protein; 1456 AA.
DE Mannose receptor polypeptide seq id 95.
PN US2003157113-A1.
PD 21-AUG-2003.
PA (TERM/) TERMAN D S.
Query Match 7.1%; Score 178.5; DB 7; Length 1456;
Best Local Similarity 29.2%; Pred. No. 0.00023;
RESULT 1370
ID ADN39899 standard; protein; 1456 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C269.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 7.1%; Score 178.5; DB 7; Length 1456;
Best Local Similarity 29.2%; Pred. No. 0.00023;
RESULT 1371
ID ADN95147 standard; protein; 1456 AA.
DE Human BEC/LEC-related protein sequence SeqID69.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 7.1%; Score 178.5; DB 7; Length 1456;
Best Local Similarity 29.2%; Pred. No. 0.00023;
RESULT 1372
ID ADL12439 standard; protein; 1456 AA.
DE Human steroid-induced C3A liver cell protein #22.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.1%; Score 178.5; DB 8; Length 1456;
Best Local Similarity 29.2%; Pred. No. 0.00023;
RESULT 1373
ID ADQ17856 standard; protein; 1456 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 673.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.1%; Score 178.5; DB 8; Length 1456;
Best Local Similarity 29.2%; Pred. No. 0.00023;
RESULT 1374
ID ADP23714 standard; protein; 1456 AA.
DE PRO polypeptide SEQ ID NO:892.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 178.5; DB 8; Length 1456;
Best Local Similarity 29.2%; Pred. No. 0.00023;
RESULT 1375
ID AAW39256 standard; protein; 612 AA.
DE Human partial mature membrane protein.
PN JP10036395-A.
PD 10-FEB-1998.
PA (ASAH) ASAHI KASEI KOGYO KK.
Query Match 7.0%; Score 178; DB 2; Length 612;
Best Local Similarity 28.7%; Pred. No. 9.4e-05;
RESULT 1376
ID ABM82843 standard; protein; 694 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3092.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.0%; Score 178; DB 8; Length 694;
Best Local Similarity 28.7%; Pred. No. 0.00011;
RESULT 1377
ID AAW39257 standard; protein; 737 AA.
DE Human membrane protein.
PN JP10036395-A.
PD 10-FEB-1998.
PA (ASAH) ASAHI KASEI KOGYO KK.
Query Match 7.0%; Score 178; DB 2; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1378
ID AAY17822 standard; protein; 737 AA.
DE Human PRO299 protein sequence.
PN WO9928462-A2.
PD 10-JUN-1999.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 2; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1379

ID AAB01313 standard; protein; 737 AA.
DE Human PRO299 polypeptide.
PN WO200032776-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 3; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1380
ID AAU29042 standard; protein; 737 AA.
DE Human PRO polypeptide sequence #19.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 4; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1381
ID AAU76235 standard; protein; 737 AA.
DE Human epidermal growth factor (EGF) motif repeat protein.
PN WO200212335-A2.
PD 14-FEB-2002.
PA (PHAA) PHARMACIA CORP.
Query Match 7.0%; Score 178; DB 5; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1382
ID ABU58418 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1383
ID ABU87966 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1384
ID ABU84281 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1385
ID ABR66155 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1386
ID ABR65545 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1387
ID ABU99485 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1388
ID ABU55922 standard; protein; 737 AA.
DE Human secreted/transmembrane protein PRO299.
PN US2002142959-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;

RESULT 1389
ID ABU82724 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1390
ID ABU89845 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1391
ID ABR68094 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1392
ID ABU96147 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1393
ID ABU92578 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1394
ID ABO08655 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1395
ID ABO02707 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1396
ID ABR74861 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1397
ID ABR94623 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1398
ID ABU60232 standard; protein; 737 AA.
DE Human PRO polypeptide #3.
PN US2002132768-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1399
ID ABU85596 standard; protein; 737 AA.

DE Human PRO polypeptide #19.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1400
ID ABU98756 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1401
ID ABU97971 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1402
ID ABU91677 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1403
ID ABU89370 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1404
ID ABU86211 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1405
ID ABU67424 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1406
ID ABU80452 standard; protein; 737 AA.
DE Human PRO protein #19.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1407
ID ABR99370 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1408
ID ABR98760 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1409
ID ABO16283 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1410
ID ABR92183 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1411
ID ABO18824 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1412
ID ABR78245 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1413
ID ABU64918 standard; protein; 737 AA.
DE Human secreted/transmembrane protein PRO299.
PN US2002173463-A1.
PD 21-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1414
ID ABU84981 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1415
ID ABO00120 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1416
ID ABO11452 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1417
ID ABO02097 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1418
ID ABU58352 standard; protein; 737 AA.
DE Novel human secreted protein PRO299.
PN US2002150976-A1.
PD 17-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1419

ID ABU88671 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1420
ID ABU83366 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1421
ID ABO06167 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1422
ID ABR59203 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1423
ID ABO09265 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1424
ID ABO19129 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1425
ID ABO11147 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1426
ID ABR66765 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1427
ID ABO15978 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1428
ID ABO13684 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1429
ID ABU57238 standard; protein; 737 AA.
DE Human PRO299 protein.
PN US2002142958-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1430
ID ABU65587 standard; protein; 737 AA.
DE Human secreted/transmembrane protein, SEQ ID 38.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1431
ID ABO07435 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1432
ID ABO03622 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1433
ID ABR67070 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1434
ID ABO15673 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1435
ID ABU55954 standard; protein; 737 AA.
DE Human secreted/transmembrane protein, PRO299.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1436
ID ABU65282 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1437
ID ABU95227 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1438
ID ABU71130 standard; protein; 737 AA.
DE Human PRO299 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1439
ID ABO07740 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003032130-A1.

PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1440
ID ABR69981 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1441
ID ABR69314 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1442
ID ABO01455 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1443
ID ABU81257 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1444
ID ABR60054 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1445
ID ABR67789 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1446
ID ABR65177 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1447
ID ABR68399 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1448
ID ABR71811 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1449
ID ABU85291 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1450
ID ABU88981 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1451
ID ABU83061 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1452
ID ABU94917 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1453
ID ABU90465 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1454
ID ABU83976 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1455
ID ABU93627 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1456
ID ABR64872 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1457
ID ABR68704 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1458
ID ABO06520 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1459
ID ABR99065 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;

Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1460
ID ABU56303 standard; protein; 737 AA.
DE Human secreted/transmembrane protein, PRO299.
PN US2002132981-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1461
ID ABU56949 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1462
ID ABU85901 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1463
ID ABU82188 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1464
ID ABU87199 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1465
ID ABU83671 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1466
ID ABO08045 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1467
ID ABU12044 standard; protein; 737 AA.
DE Human NOV2a CG59843-01 protein SEQ ID 8.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1468
ID ABU60343 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2002168715-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1469
ID ABU81756 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1470
ID ABU65920 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1471
ID ABR59749 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1472
ID ABU93937 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1473
ID ABU99790 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1474
ID ABR66460 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1475
ID ABR90878 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1476
ID ABU94305 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1477
ID ABU79187 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1478
ID ABU86516 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1479
ID ABU86821 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1480

ID ABU94610 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1481
ID ABO04537 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1482
ID ABR70286 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1483
ID ABU98451 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1484
ID ABR65850 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1485
ID ABR64567 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1486
ID ABU79492 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1487
ID ABU92883 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1488
ID ABU95842 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1489
ID ABU91062 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1490
ID ABU90155 standard; protein; 737 AA.
DE Novel human secreted and transmembrane protein PRO299.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1491
ID ABO09570 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1492
ID ABO10842 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1493
ID ABR70896 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1494
ID ABU87504 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1495
ID ABU91372 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1496
ID ABU84586 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1497
ID ABR69676 standard; protein; 737 AA.
DE Human secreted polypeptide PRO299, SEQ ID NO:38.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1498
ID ABU80053 standard; protein; 737 AA.
DE Human PRO protein #19.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1499
ID ABU93322 standard; protein; 737 AA.
DE Human PRO polypeptide #19.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;
Best Local Similarity 28.7%; Pred. No. 0.00012;
RESULT 1500
ID ABO09875 standard; protein; 737 AA.
DE Human secreted/transmembrane protein (PRO) #19.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 7.0%; Score 178; DB 6; Length 737;

Best Local Similarity 28.7%; Pred. No. 0.00012;

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